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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:50:07 ; Search time 19 Seconds
(without alignments)
910.247 Million cell up

Title: US-10-063-549-46

Perfect score: 335

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Listing first 700 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	8	2.4	360	4	US-09-907-794A-213	Sequence 213, App
2	8	2.4	360	4	US-09-905-125A-213	Sequence 213, App
3	8	2.4	360	4	US-09-902-775A-213	Sequence 213, App
4	8	2.4	410	4	US-09-252-991A-31174	Sequence 31174, A
5	7	2.1	63	4	US-09-646-691B-10	Sequence 10, Appl
6	7	2.1	67	4	US-09-543-681A-4733	Sequence 4733, Ap
7	7	2.1	97	4	US-09-886-319A-29	Sequence 29, Appl
8	7	2.1	98	3	US-08-613-823-A	Sequence 4, Appl
9	7	2.1	98	3	US-08-852-213-2	Sequence 2, Appl
10	7	2.1	98	4	US-09-479-723B-4	Sequence 4, Appl
11	7	2.1	98	4	US-09-261-201A-4	Sequence 4, Appl
12	7	2.1	98	4	US-09-717-209-A	Sequence 2, Appl
13	7	2.1	98	4	US-09-545-894-2	Sequence 2, Appl
14	7	2.1	192	3	US-08-486-099-107	Sequence 107, App
15	7	2.1	192	3	US-08-360-107A-117	Sequence 117, App
16	7	2.1	192	3	US-08-484-223B-107	Sequence 107, App
17	7	2.1	192	3	US-08-919-597-107	Sequence 107, App
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23	7	2.1	192	4	US-08-470-896-107	Sequence 107, App
24	7	2.1	192	4	US-08-485-546A-107	Sequence 107, App
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26	7	2.1	208	3	US-09-092-409-72	Sequence 72, Appl
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296	6	1.8	204	4	US-09-134-000C-3913	Sequence 3913, Ap	369	6	272	3	US-09-570-367C-19	Sequence 19, Appl
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300	6	1.8	206	4	US-09-562-737-57	Sequence 57, Appl	373	6	274	6	5489533-2	Patent No. 5489533
301	6	1.8	206	4	US-09-562-737-58	Sequence 58, Appl	374	6	274	6	5512660-2	Patent No. 5512660
302	6	1.8	206	4	US-09-562-737-59	Sequence 59, Appl	375	6	278	4	US-09-570-367C-2	Sequence 2, Appl
303	6	1.8	206	4	US-09-562-737-59	Sequence 59, Appl	376	6	278	4	US-09-570-367C-21	Sequence 21, Appl
304	6	1.8	209	3	US-08-235-836C-32	Sequence 32, Appl	377	6	278	4	US-09-915-524-2	Sequence 2, Appl
305	6	1.8	210	4	US-09-697-367-10	Sequence 10, Appl	378	6	278	4	US-09-915-524-21	Sequence 21, Appl
306	6	1.8	210	4	US-09-134-001C-4790	Sequence 4790, Ap	379	6	282	4	US-09-247-890-16	Sequence 16, Appl
307	6	1.8	211	4	US-09-252-991A-25965	Sequence 25965, A	380	6	282	4	US-09-724-969-16	Sequence 16, Appl
308	6	1.8	212	1	US-08-158-353-4	Sequence 4, Appl	381	6	282	4	US-09-724-852-16	Sequence 16, Appl
309	6	1.8	212	2	US-08-763-121-1	Sequence 1, Appl	382	6	282	4	US-09-134-000C-4468	Sequence 4468, Ap
310	6	1.8	212	3	US-09-196-293-11	Sequence 11, Appl	383	6	283	4	US-09-904-615-106	Sequence 106, Ap
311	6	1.8	212	3	US-08-209-603E-11	Sequence 11, Appl	384	6	287	4	US-09-310-463-32	Sequence 32, Appl
312	6	1.8	212	3	US-08-235-836C-34	Sequence 34, Appl	385	6	287	4	US-09-252-991A-30447	Sequence 30447, A
313	6	1.8	212	4	US-09-216-066-1	Sequence 1, Appl	386	6	288	4	US-09-489-039A-14187	Sequence 14187, A
314	6	1.8	212	4	US-09-711-546-11	Sequence 11, Appl	387	6	288	4	US-09-489-039A-12218	Sequence 12218, A
315	6	1.8	213	2	US-08-763-121-3	Sequence 3, Appl	388	6	293	4	US-09-252-991A-26267	Sequence 26267, A
316	6	1.8	213	4	US-09-216-066-3	Sequence 3, Appl	389	6	297	4	US-09-632-947B-4	Sequence 4, Appl
317	6	1.8	214	4	US-09-187-789-9	Sequence 9, Appl	390	6	298	4	US-09-232-160-17	Sequence 17, Appl
318	6	1.8	216	4	US-09-489-039A-7265	Sequence 7265, Ap	391	6	298	4	US-09-252-991A-23700	Sequence 23700, A
319	6	1.8	217	4	US-09-690-454-196	Sequence 196, Ap	392	6	298	4	US-09-800-729-87	Sequence 87, Appl

393	6	1.8	298	4	US-09-800-729-121	Sequence 121, Appl	455	6	1.8	352	2	US-08-933-750C-46	Sequence 46, Appl
394	6	1.8	298	4	US-09-582-934-2	Sequence 2, Appl	456	6	1.8	352	3	US-09-234-613-46	Sequence 46, Appl
395	6	1.8	299	4	US-09-310-463-30	Sequence 30, Appl	457	6	1.8	353	4	US-09-252-991A-25209	Sequence 25209, A
396	6	1.8	300	4	US-09-543-681A-6670	Sequence 6670, Ap	458	6	1.8	353	4	US-09-543-681A-7190	Sequence 7190, Ap
397	6	1.8	301	4	US-09-107-532A-4953	Sequence 4953, Ap	459	6	1.8	354	2	US-08-394-189B-20	Sequence 20, Appl
398	6	1.8	301	4	US-09-582-934-1	Sequence 1, Appl	460	6	1.8	354	2	US-09-198-452A-526	Sequence 526, App
399	6	1.8	302	4	US-09-874-923-122	Sequence 122, App	471	6	1.8	355	4	US-09-934-901-8	Sequence 8, Appl
400	6	1.8	303	1	US-08-185-432-5	Sequence 5, Appl	472	6	1.8	358	4	US-09-668-097A-36	Sequence 36, Appl
401	6	1.8	304	4	US-09-632-947B-7	Sequence 7, Appl	473	6	1.8	361	4	US-09-134-001C-5403	Sequence 5403, Ap
402	6	1.8	304	4	US-09-489-039A-11906	Sequence 11906, A	474	6	1.8	362	4	US-09-252-991A-18016	Sequence 18016, A
403	6	1.8	305	4	US-09-540-236-3603	Sequence 3603, Ap	475	6	1.8	363	4	US-09-252-991A-25052	Sequence 25052, A
404	6	1.8	308	4	US-09-252-991A-20337	Sequence 20337, A	476	6	1.8	363	4	US-09-205-258-1008	Sequence 1008, Ap
405	6	1.8	309	1	US-08-729-202-1	Sequence 1, Appl	477	6	1.8	364	4	US-09-417-485D-49	Sequence 49, Appl
406	6	1.8	309	1	US-08-896-371-1	Sequence 1, Appl	478	6	1.8	364	4	US-09-724-224-2	Sequence 2, Appl
407	6	1.8	309	3	US-08-996-338-22	Sequence 22, Appl	479	6	1.8	370	4	US-08-225-477B-8	Sequence 8, Appl
408	6	1.8	309	4	US-09-556-972-22	Sequence 22, Appl	480	6	1.8	371	1	US-09-148-545-359	Sequence 259, App
409	6	1.8	310	4	US-09-252-991A-16914	Sequence 16914, A	481	6	1.8	371	5	PCT-US95-04353-8	Sequence 8, Appl
410	6	1.8	311	4	US-09-222-939-8	Sequence 8, Appl	482	6	1.8	371	5	US-09-071-035-102	Sequence 102, App
411	6	1.8	311	4	US-09-252-991A-28068	Sequence 28068, A	483	6	1.8	372	4	US-09-252-991A-28586	Sequence 28586, A
412	6	1.8	311	4	US-09-543-681A-4963	Sequence 4963, Ap	484	6	1.8	372	4	US-08-232-931A-30132	Sequence 30132, A
413	6	1.8	311	4	US-10-023-528-8	Sequence 8, Appl	485	6	1.8	372	4	US-08-888-077A-16	Sequence 16, Appl
414	6	1.8	312	2	US-08-808-931-22	Sequence 22, Appl	486	6	1.8	373	3	US-09-665-479A-16	Sequence 27, Appl
415	6	1.8	312	3	US-08-808-931-22	Sequence 22, Appl	487	6	1.8	377	4	US-08-225-477B-9	Sequence 9, Appl
416	6	1.8	312	3	US-09-050-603A-22	Sequence 22, Appl	488	6	1.8	378	1	PCT-US95-04353-9	Sequence 9, Appl
417	6	1.8	312	3	US-09-102-420B-22	Sequence 22, Appl	489	6	1.8	378	5	US-09-489-039A-11991	Sequence 11991, A
418	6	1.8	312	4	US-09-497-698-22	Sequence 22, Appl	490	6	1.8	379	4	US-09-029-333-2	Sequence 2, Appl
419	6	1.8	312	4	US-09-107-532A-6219	Sequence 6219, Ap	491	6	1.8	382	4	US-08-946-026-27	Sequence 27, Appl
420	6	1.8	313	3	US-09-347-803-25	Sequence 25, Appl	492	6	1.8	384	3	US-08-123-161A-10	Sequence 10, Appl
421	6	1.8	313	4	US-09-252-991A-22411	Sequence 22411, A	493	6	1.8	386	4	US-08-123-161A-12	Sequence 12, Appl
422	6	1.8	313	4	US-09-252-991A-24305	Sequence 24305, A	494	6	1.8	387	1	US-08-483-278-10	Sequence 10, Appl
423	6	1.8	314	4	US-09-107-532A-4919	Sequence 4919, Ap	495	6	1.8	387	1	US-08-483-278-12	Sequence 12, Appl
424	6	1.8	315	1	US-07-757-390-8	Sequence 8, Appl	496	6	1.8	387	1	US-08-134-001C-3625	Sequence 3625, Ap
425	6	1.8	315	1	US-08-442-282-8	Sequence 8, Appl	497	6	1.8	387	1	US-07-817-920-6	Sequence 6, Appl
426	6	1.8	315	1	US-08-442-281-8	Sequence 8, Appl	498	6	1.8	390	1	US-08-216-594-6	Sequence 6, Appl
427	6	1.8	315	2	US-08-939-727-8	Sequence 8, Appl	499	6	1.8	390	1	US-08-461-812-4	Sequence 4, Appl
428	6	1.8	315	4	US-09-252-991A-25763	Sequence 25763, A	500	6	1.8	390	2	US-08-157-185-15	Sequence 15, Appl
429	6	1.8	316	4	US-09-252-991A-18829	Sequence 18829, A	501	6	1.8	390	2	US-08-281-526B-15	Sequence 15, Appl
430	6	1.8	317	4	US-09-252-991A-22489	Sequence 22489, A	502	6	1.8	390	2	US-09-450-790A-15	Sequence 15, Appl
431	6	1.8	318	4	US-09-134-001C-3852	Sequence 3852, Ap	503	6	1.8	390	3	US-09-332-837-15	Sequence 15, Appl
432	6	1.8	319	4	US-09-134-000C-5242	Sequence 5242, Ap	504	6	1.8	390	4	PCT-US93-00149-6	Sequence 4, Appl
433	6	1.8	324	4	US-09-252-991A-24664	Sequence 24664, A	505	6	1.8	390	4	US-09-543-681A-6203	Sequence 6203, Ap
434	6	1.8	329	1	US-08-225-477B-3	Sequence 3, Appl	506	6	1.8	398	1	US-07-757-390-6	Sequence 6, Appl
435	6	1.8	329	2	US-08-562-535C-4	Sequence 4, Appl	507	6	1.8	398	1	US-08-442-282-6	Sequence 6, Appl
436	6	1.8	329	2	US-08-743-605D-4	Sequence 4, Appl	508	6	1.8	398	1	US-08-442-281-6	Sequence 6, Appl
437	6	1.8	329	3	US-09-259-294-4	Sequence 4, Appl	509	6	1.8	398	2	US-08-939-727-6	Sequence 6, Appl
438	6	1.8	329	4	US-09-489-039A-10276	Sequence 10276, A	510	6	1.8	398	3	US-09-088-351-6	Sequence 6, Appl
439	6	1.8	329	5	PCT-US95-04353-3	Sequence 3, Appl	511	6	1.8	398	4	US-09-328-352-6411	Sequence 6411, Ap
440	6	1.8	331	1	US-08-356-180-3	Sequence 3, Appl	512	6	1.8	399	4	US-09-134-000C-4500	Sequence 4500, Ap
441	6	1.8	332	1	US-07-757-390-7	Sequence 7, Appl	513	6	1.8	399	4	US-09-252-991A-31178	Sequence 31178, A
442	6	1.8	332	1	US-08-442-281-7	Sequence 7, Appl	514	6	1.8	402	4	US-09-134-001C-3544	Sequence 3544, Ap
443	6	1.8	332	1	US-08-442-281-7	Sequence 7, Appl	515	6	1.8	406	4	US-09-258-754-449	Sequence 449, App
444	6	1.8	332	2	US-08-939-727-7	Sequence 7, Appl	516	6	1.8	409	3	US-09-252-991A-22340	Sequence 22340, A
445	6	1.8	333	4	US-09-198-452A-652	Sequence 652, App	517	6	1.8	410	4	US-09-543-681A-7404	Sequence 7404, Ap
446	6	1.8	334	4	US-09-252-991A-18120	Sequence 18120, A	518	6	1.8	411	4	US-08-349-696-21	Sequence 21, Appl
447	6	1.8	334	4	US-09-252-991A-22395	Sequence 22395, A	519	6	1.8	412	1	US-08-233-009-21	Sequence 21, Appl
448	6	1.8	335	1	US-07-947-130-3	Sequence 3, Appl	520	6	1.8	412	1	US-08-560-231-21	Sequence 21, Appl
449	6	1.8	335	1	US-08-421-822-3	Sequence 3, Appl	521	6	1.8	412	2	US-09-080-704A-21	Sequence 21, Appl
450	6	1.8	335	1	US-08-421-822-3	Sequence 3, Appl	522	6	1.8	412	3	US-09-800-274-5	Sequence 5, Appl
451	6	1.8	335	4	US-09-543-681A-7733	Sequence 7733, Ap	523	6	1.8	414	4	US-09-252-991A-20866	Sequence 20866, A
452	6	1.8	337	2	US-09-013-634-2	Sequence 7, Appl	524	6	1.8	414	4	US-09-543-681A-4320	Sequence 4320, Ap
453	6	1.8	340	4	US-09-543-681A-5967	Sequence 5967, Ap	525	6	1.8	414	4	US-09-489-039A-10428	Sequence 10428, A
454	6	1.8	342	4	US-09-071-035-104	Sequence 104, App	526	6	1.8	415	1	US-07-757-390-5	Sequence 5, Appl
455	6	1.8	344	3	US-09-110-116-4	Sequence 4, Appl	527	6	1.8	415	1	US-08-442-282-5	Sequence 5, Appl
456	6	1.8	345	4	US-09-252-991A-16669	Sequence 16669, A	528	6	1.8	415	2	US-08-939-727-5	Sequence 5, Appl
457	6	1.8	346	4	US-09-724-224-6	Sequence 2, Appl	529	6	1.8	415	4	US-09-886-319A-23	Sequence 23, Appl
458	6	1.8	346	5	PCT-US96-10602-2	Sequence 6, Appl	530	6	1.8	417	4	US-09-489-039A-12272	Sequence 12272, A
459	6	1.8	347	3	US-08-857-076-100	Sequence 100, App	531	6	1.8				
460	6	1.8	349	1	US-08-118-270-7	Sequence 7, Appl	532	6	1.8				
461	6	1.8	349	5	PCT-US93-08528-7	Sequence 7, Appl	533	6	1.8				
462	6	1.8	350	4	US-09-161-241-9	Sequence 9, Appl	534	6	1.8				
463	6	1.8	350	4	US-09-907-794A-236	Sequence 236, App	535	6	1.8				
464	6	1.8	350	4	US-09-905-135A-236	Sequence 236, App	536	6	1.8				
465	6	1.8	350	4	US-09-902-775A-236	Sequence 236, App	537	6	1.8				

539	6	1.8	419	3	US-08-974-691-3	Sequence 3, Appli	612	6	1.8	487	4	US-09-489-039A-12980	Sequence 12980, A
540	6	1.8	420	4	US-09-705-448-10	Sequence 10, Appl	613	6	1.8	489	4	US-08-983-502-9	Sequence 9, Appli
541	6	1.8	421	4	US-09-543-681A-7791	Sequence 7791, Ap	614	6	1.8	489	4	US-09-516-747-9	Sequence 9, Appli
542	6	1.8	422	2	US-08-290-731C-10	Sequence 10, Appl	615	6	1.8	489	5	PCT-US96-10521-9	Sequence 9, Appli
543	6	1.8	423	2	US-08-290-731C-11	Sequence 11, Appl	616	6	1.8	495	4	US-09-328-352-4637	Sequence 4637, Ap
544	6	1.8	424	3	US-08-855-910-13	Sequence 13, Appl	617	6	1.8	500	4	US-09-107-532A-4085	Sequence 4085, Ap
545	6	1.8	425	4	US-09-328-352-4199	Sequence 4199, Ap	618	6	1.8	503	2	US-08-394-189B-2	Sequence 2, Appli
546	6	1.8	426	4	US-09-252-991A-20025	Sequence 20025, A	619	6	1.8	503	2	US-08-258-287B-2	Sequence 2, Appli
547	6	1.8	427	4	US-09-134-000C-5142	Sequence 5142, Ap	620	6	1.8	503	3	US-08-258-287B-35	Sequence 35, Appl
548	6	1.8	428	4	US-08-566-171E-5244	Sequence 5244, Ap	621	6	1.8	503	3	US-08-258-287B-36	Sequence 36, Appl
549	6	1.8	429	4	US-09-252-991A-20728	Sequence 20728, A	622	6	1.8	503	3	US-08-368-704C-2	Sequence 2, Appli
550	6	1.8	430	4	US-09-252-991A-22081	Sequence 22081, A	623	6	1.8	503	3	US-08-368-704C-35	Sequence 35, Appl
551	6	1.8	431	4	US-09-252-991A-32048	Sequence 32048, A	624	6	1.8	503	3	US-08-368-704C-36	Sequence 36, Appl
552	6	1.8	432	2	US-08-808-931-24	Sequence 24, Appl	625	6	1.8	503	3	US-08-740-223A-11	Sequence 11, Appl
553	6	1.8	433	4	US-08-808-323-24	Sequence 24, Appl	626	6	1.8	503	4	US-09-709-188-11	Sequence 11, Appl
554	6	1.8	434	3	US-09-050-603A-24	Sequence 24, Appl	627	6	1.8	503	4	US-08-724-378D-10	Sequence 10, Appl
555	6	1.8	435	4	US-09-102-420B-24	Sequence 24, Appl	628	6	1.8	503	4	US-08-999-689A-6	Sequence 6, Appli
556	6	1.8	436	4	US-09-497-698-24	Sequence 24, Appl	629	6	1.8	503	4	US-09-291-283-12	Sequence 12, Appl
557	6	1.8	437	4	US-09-252-991A-30607	Sequence 30607, A	630	6	1.8	503	5	PCT-US93-05701-19	Sequence 19, Appl
558	6	1.8	438	4	US-09-489-039A-12786	Sequence 12786, A	631	6	1.8	503	5	PCT-US93-05705-2	Sequence 2, Appli
559	6	1.8	439	4	US-09-489-039A-9246	Sequence 9246, Ap	632	6	1.8	505	2	US-08-394-189B-5	Sequence 5, Appli
560	6	1.8	440	4	US-09-328-352-5528	Sequence 5528, Ap	633	6	1.8	505	5	PCT-US93-05701-20	Sequence 20, Appl
561	6	1.8	441	2	US-07-914-373C-22	Sequence 22, Appl	634	6	1.8	505	5	PCT-US93-05705-5	Sequence 5, Appli
562	6	1.8	442	3	US-08-437-642B-22	Sequence 22, Appl	635	6	1.8	507	4	US-09-252-991A-23432	Sequence 23432, A
563	6	1.8	443	3	US-08-929-329-8	Sequence 8, Appli	636	6	1.8	509	2	US-08-665-926-8	Sequence 8, Appli
564	6	1.8	444	4	US-08-146-206C-22	Sequence 22, Appl	637	6	1.8	509	3	US-08-740-223A-10	Sequence 10, Appl
565	6	1.8	445	4	US-09-705-686-22	Sequence 22, Appl	638	6	1.8	509	4	US-09-202-491-2	Sequence 2, Appli
566	6	1.8	446	5	PCT-US93-07832-22	Sequence 22, Appl	639	6	1.8	509	4	US-09-202-491-3	Sequence 3, Appli
567	6	1.8	447	4	US-09-540-236-2135	Sequence 2325, Ap	640	6	1.8	509	4	US-09-709-188-10	Sequence 10, Appl
568	6	1.8	448	4	US-09-328-352-6174	Sequence 6174, Ap	641	6	1.8	509	4	US-09-328-352-6488	Sequence 6488, Ap
569	6	1.8	449	3	US-08-870-518-4	Sequence 4, Appli	642	6	1.8	510	1	US-08-278-635B-4	Sequence 4, Appli
570	6	1.8	450	2	US-08-836-567-4	Sequence 4, Appli	643	6	1.8	510	3	US-08-471-961-4	Sequence 4, Appli
571	6	1.8	451	4	US-09-606-304-4	Sequence 4, Appli	644	6	1.8	510	4	US-09-345-109C-4	Sequence 4, Appli
572	6	1.8	452	4	US-09-647-540A-2	Sequence 2, Appli	645	6	1.8	511	3	US-08-464-258B-4	Sequence 4, Appli
573	6	1.8	453	4	US-10-119-600-2	Sequence 2, Appli	646	6	1.8	512	4	US-09-724-224-4	Sequence 4, Appli
574	6	1.8	454	4	US-09-198-452A-7	Sequence 7, Appli	647	6	1.8	514	3	US-08-999-689A-7	Sequence 7, Appli
575	6	1.8	455	4	US-10-119-651-2	Sequence 2, Appli	648	6	1.8	514	3	US-08-688-988-35	Sequence 35, Appl
576	6	1.8	456	2	US-08-865-597A-2	Sequence 2, Appli	649	6	1.8	515	2	US-09-073-362-3	Sequence 3, Appli
577	6	1.8	457	4	US-09-252-991A-29065	Sequence 29065, A	650	6	1.8	515	2	US-09-243-920-3	Sequence 3, Appli
578	6	1.8	458	4	US-09-489-039A-13721	Sequence 13721, A	651	6	1.8	516	4	US-09-252-991A-29719	Sequence 29719, A
579	6	1.8	459	1	US-07-882-202A-4	Sequence 4, Appli	652	6	1.8	517	3	US-09-282-305-8	Sequence 8, Appli
580	6	1.8	460	1	US-08-021-615A-4	Sequence 4, Appli	653	6	1.8	517	4	US-09-883-720-8	Sequence 8, Appli
581	6	1.8	461	3	US-08-321-777-4	Sequence 4, Appli	654	6	1.8	520	4	US-09-068-740A-3	Sequence 3, Appli
582	6	1.8	462	3	US-09-009-217-14	Sequence 14, Appl	655	6	1.8	520	4	US-09-527-073-2	Sequence 2, Appli
583	6	1.8	463	3	US-09-009-656-14	Sequence 14, Appl	656	6	1.8	521	2	US-08-878-563A-3	Sequence 3, Appli
584	6	1.8	464	5	PCT-US93-04493-4	Sequence 4, Appli	657	6	1.8	521	3	US-08-996-338-20	Sequence 20, Appl
585	6	1.8	465	3	US-09-086-483A-6	Sequence 6, Appli	658	6	1.8	521	3	US-09-270-117-3	Sequence 3, Appli
586	6	1.8	466	4	US-09-580-212-6	Sequence 6, Appli	659	6	1.8	521	3	US-08-956-322-4	Sequence 4, Appli
587	6	1.8	467	4	US-09-273-871A-11	Sequence 11, Appl	660	6	1.8	521	3	US-09-252-991A-30623	Sequence 30623, A
588	6	1.8	468	4	US-09-769-402-6	Sequence 6, Appli	661	6	1.8	521	4	US-09-556-972-20	Sequence 20, Appl
589	6	1.8	469	4	US-09-013-895A-2	Sequence 2, Appli	662	6	1.8	521	4	US-09-046-572-5	Sequence 5, Appli
590	6	1.8	470	4	US-09-134-001C-3999	Sequence 3999, Ap	663	6	1.8	522	4	US-09-198-452A-480	Sequence 480, App
591	6	1.8	471	4	US-09-565-918-2	Sequence 2, Appli	664	6	1.8	526	4	US-09-252-991A-27044	Sequence 27044, A
592	6	1.8	472	4	US-09-448-868-2	Sequence 2, Appli	665	6	1.8	528	2	US-08-808-931-10	Sequence 10, Appl
593	6	1.8	473	4	US-10-039-785-1	Sequence 1, Appli	666	6	1.8	528	3	US-08-808-323-10	Sequence 10, Appl
594	6	1.8	474	4	US-09-328-352-5724	Sequence 5724, Ap	667	6	1.8	528	3	US-09-050-603A-10	Sequence 10, Appl
595	6	1.8	475	4	US-09-540-236-3598	Sequence 3598, Ap	668	6	1.8	528	3	US-09-102-420B-10	Sequence 10, Appl
596	6	1.8	476	4	US-09-489-039A-10571	Sequence 10571, A	669	6	1.8	528	4	US-09-497-698-10	Sequence 10, Appl
597	6	1.8	477	4	US-09-540-236-2232	Sequence 2292, Ap	670	6	1.8	528	4	US-09-010-147B-20	Sequence 20, Appl
598	6	1.8	478	1	US-08-472-028A-6	Sequence 6, Appli	671	6	1.8	531	4	US-09-489-039A-3781	Sequence 3781, Ap
599	6	1.8	479	2	US-08-808-931-6	Sequence 6, Appli	672	6	1.8	535	4	US-09-252-991A-31062	Sequence 31062, A
600	6	1.8	480	3	US-08-808-323-6	Sequence 6, Appli	673	6	1.8	536	3	US-08-808-931-20	Sequence 20, Appl
601	6	1.8	481	3	US-09-050-603A-6	Sequence 6, Appli	674	6	1.8	536	3	US-08-808-323-20	Sequence 20, Appl
602	6	1.8	482	3	US-09-102-420B-6	Sequence 6, Appli	675	6	1.8	536	3	US-09-050-603A-20	Sequence 20, Appl
603	6	1.8	483	3	US-09-015-683-6	Sequence 6, Appli	676	6	1.8	536	3	US-09-102-420B-20	Sequence 20, Appl
604	6	1.8	484	4	US-09-497-698-6	Sequence 6, Appli	677	6	1.8	536	4	US-09-497-698-20	Sequence 20, Appl
605	6	1.8	485	3	US-09-071-296-6	Sequence 6, Appli	678	6	1.8	537	4	US-09-328-352-4594	Sequence 4594, Ap
606	6	1.8	486	3	US-09-196-268-6	Sequence 6, Appli	679	6	1.8	537	1	US-08-472-028A-2	Sequence 2, Appli
607	6	1.8	487	4	US-09-191-998-6	Sequence 6, Appli	680	6	1.8	537	3	US-08-808-931-2	Sequence 2, Appli
608	6	1.8	488	4	US-09-328-352-4849	Sequence 4849, Ap	681	6	1.8	537	3	US-08-808-323-2	Sequence 2, Appli
609	6	1.8	489	4	US-09-724-224-8	Sequence 8, Appli	682	6	1.8	537	3	US-09-050-603A-2	Sequence 2, Appli
610	6	1.8	490	4	US-09-620-412C-349	Sequence 349, App	683	6	1.8	537	3	US-09-102-420B-2	Sequence 2, Appli
611	6	1.8	491	4	US-09-598-419-349	Sequence 349, App	684	6	1.8	537	3	US-09-071-296-2	Sequence 2, Appli

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Sequence 16, Appli
Sequence 16, Appli
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Sequence 2, Appli
Sequence 28, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 12, Appli

6 1.8 537 3 US-09-196-268-2
6 1.8 537 3 US-09-015-683-2
6 1.8 537 4 US-09-191-998-2
6 1.8 537 4 US-09-497-698-2
6 1.8 539 2 US-08-808-931-16
6 1.8 539 3 US-08-808-323-16
6 1.8 539 3 US-09-050-603A-16
6 1.8 539 3 US-09-102-420B-16
6 1.8 539 4 US-09-497-698-16
6 1.8 541 1 US-08-604-333-2
6 1.8 541 3 US-09-110-618-2
6 1.8 541 4 US-09-173-151A-28
6 1.8 541 4 US-09-578-178-2
6 1.8 541 4 US-09-577-806-2
6 1.8 541 4 US-09-621-502-4
6 1.8 543 2 US-08-808-931-12

ALIGNMENTS

RESULT 1
US-09-907-794A-213
; Sequence 213, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 231 LLLVPLLL 238
Db 4 LLLVPLLL 11
|||||

RESULT 2

US-09-905-125A-213
; Sequence 213, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-213

Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 LLLVPLLL 238
DB 4 LLLVPLLL 11

RESULT 3
US-09-902-775A-213
; Sequence 213, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 213
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-213
Query Match 2.4%; Score 8; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 LLLVPLLL 238
DB 4 LLLVPLLL 11
RESULT 4
US-09-252-991A-31174
; Sequence 31174, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 31174
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31174

  Query Match          2.1%; Score 8; DB 4; Length 410;
  Best Local Similarity 100.0%; Pred. No. 18;
  Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LVGSVCGA 36
Db 312 LVGSVCGA 319

RESULT 5
US-09-646-691B-10
; Sequence 10, Application US/09646691B
; Patent No. 6642353
; GENERAL INFORMATION:
; APPLICANT: McCONNELL, Stephen, J. and SPINELLA, Dominic, G.
; TITLE OF INVENTION: PEPTIDE LIGANDS FOR THE ERYTHROPOIETIN
; RECEPTOR
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 10210 Genetic Center Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/646,691B
; FILING DATE: 20-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gritzmacher, Christine A
; REGISTRATION NUMBER: 40,627
; REFERENCE/DOCKET NUMBER: CB9701-A01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-410-8926
; TELEFAX: 619-410-8928
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6642353e
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-646-691B-10

  Query Match          2.1%; Score 7; DB 4; Length 63;
  Best Local Similarity 100.0%; Pred. No. 31;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGSAAAG 24
Db 37 TGSAAAG 43

RESULT 6
US-09-543-681A-4733
; Sequence 4733, Application US/09543681A
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; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4733
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4733

  Query Match          2.1%; Score 7; DB 4; Length 67;
  Best Local Similarity 100.0%; Pred. No. 33;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LLSLFLV 243
Db 60 LLSLFLV 66

RESULT 7
US-09-886-319A-29
; Sequence 29, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; the Diagnosis or Treatment of Skin Disorders and Wound
; Healing and for the Identification of Pharmacologically
; Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-29

  Query Match          2.1%; Score 7; DB 4; Length 97;
  Best Local Similarity 100.0%; Pred. No. 45;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLCLLL 233
Db 6 VLCLLL 12

RESULT 8
US-08-613-822-4
; Sequence 4, Application US/08613822
; Patent No. 6174995
; GENERAL INFORMATION:
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Human Chemokine Polypeptides
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,822
FILING DATE: 23-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Millstein, Larry S
REGISTRATION NUMBER: 34,679
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-613-822-4

Query Match 2.1%; Score 7; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
Db 6 VLLCLLL 12

RESULT 9
US-08-852-212-2
Sequence 2, Application US/08852212
Patent No. 6290948
GENERAL INFORMATION:
APPLICANT: White et al.
TITLE OF INVENTION: Method of Treating Sepsis and ARDS using Chemokine Beta-10
CURRENT APPLICATION NUMBER: US/08/852,212
CURRENT FILING DATE: 1997-05-06
EARLIER APPLICATION NUMBER: 60/017,871
EARLIER FILING DATE: 1996-05-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-08-852-212-2

Query Match 2.1%; Score 7; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
Db 6 VLLCLLL 12

RESULT 10
US-09-479-729B-4
Sequence 4, Application US/09479729B
Patent No. 6391589
GENERAL INFORMATION:
APPLICANT: Olsen, et al

TITLE OF INVENTION: Human Chemokine Beta-10 Mutant Polypeptides
FILE REFERENCE: PF504
CURRENT APPLICATION NUMBER: US/09/479,729B
CURRENT FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: PCT/US94/09484
PRIOR FILING DATE: 1994-08-23
PRIOR APPLICATION NUMBER: 08/458,355
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: 08/462,967
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 60/115,439
PRIOR FILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-09-479-729B-4

Query Match 2.1%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
Db 6 VLLCLLL 12

RESULT 11
US-09-261-201A-4
Sequence 4, Application US/09261201A
Patent No. 6458349
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Polynucleotides Encoding Chemokine B-4
FILE REFERENCE: PFI32PDI1
CURRENT APPLICATION NUMBER: US/09/261,201A
CURRENT FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: 08/458,355
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/09484
PRIOR FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-09-261-201A-4

Query Match 2.1%; Score 7; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
Db 6 VLLCLLL 12

RESULT 12
US-09-717-209-4
Sequence 4, Application US/09717209
Patent No. 6673344
GENERAL INFORMATION:
APPLICANT: Li, Haodong
TITLE OF INVENTION: Human Chemokine Polypeptides
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD

1 COUNTRY: USA
2 ZIP: 20850
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0, Version #1.30
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/09/717,209
10 FILING DATE:
11 CLASSIFICATION:
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US/08/613,822
14 FILING DATE: 23-FEB-1996
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Millstein, Larry S
17 REGISTRATION NUMBER: 34,679
18 TELEPHONE: 301-309-8504
19 TELEFAX: 301-309-8512
20 INFORMATION FOR SEQ ID NO: 4:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 98 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: protein
26 US-09-717-209-4
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28 Query Match 2.1%; Score 7; DB 4; Length 98;
29 Best Local Similarity 100.0%; Pred. No. 46;
30 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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32 QY 227 VLLCILL 233
33 Db 6 VLLCILL 12
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35 RESULT 13
36 US-09-545-894-2
37 Sequence 2, Application US/09545894
38 Patent No. 6673915
39 GENERAL INFORMATION:
40 APPLICANT: Luster, Andrew D.
41 Sarafi, Windy N
42 Garcia-Zepeda, Eduardo A.
43 TITLE OF INVENTION: MCP-4 AND MCP-5: NOVEL CHEMOKINES
44 NUMBER OF SEQUENCES: 30
45 CORRESPONDENCE ADDRESS:
46 ADDRESSEE: Clark & Elbing LLP
47 STREET: 176 Federal Street
48 CITY: Boston
49 STATE: MA
50 COUNTRY: USA
51 ZIP: 02110
52 COMPUTER READABLE FORM:
53 MEDIUM TYPE: Diskette
54 COMPUTER: IBM Compatible
55 OPERATING SYSTEM: DOS
56 SOFTWARE: FastSeq for Windows Version 2.0
57 CURRENT APPLICATION DATA:
58 APPLICATION NUMBER: US/09/545,894
59 FILING DATE: 07-Apr-2000
60 CLASSIFICATION: <Unknown>
61 PRIOR APPLICATION DATA:
62 APPLICATION NUMBER: US/08/940,687
63 FILING DATE: 30-SEP-1997
64 APPLICATION NUMBER: 60/027,128
65 FILING DATE: 30-SEP-1996
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Bieker-Brady, Kristina
68 REGISTRATION NUMBER: 39,109
69 REFERENCE/DOCKET NUMBER: 00786/293002
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: 617-428-0200
72 TELEFAX: 617-428-7045
73 TELEX: <Unknown>
74 INFORMATION FOR SEQ ID NO: 2:
75 SEQUENCE CHARACTERISTICS:
76 LENGTH: 98 amino acids
77 TYPE: amino acid
78 STRANDEDNESS: unknown
79 TOPOLOGY: linear
80 MOLECULE TYPE: protein
81 US-09-545-894-2
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88 Db 6 VLLCILL 12
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90 RESULT 14
91 US-08-486-099-107
92 Sequence 107, Application US/08486099
93 Patent No. 6013263
94 GENERAL INFORMATION:
95 APPLICANT: Bolognesi, Dani P.
96 APPLICANT: Matthews, Thomas J.
97 APPLICANT: Wild, Carl T.
98 APPLICANT: Barney, Shawn O.
99 APPLICANT: Lambert, Dennis M.
100 APPLICANT: Petteway, Stephen R.
101 APPLICANT: Langlois, Alphonse J.
102 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
103 TITLE OF INVENTION: B VIRUS TRANSMISSION
104 NUMBER OF SEQUENCES: 209
105 CORRESPONDENCE ADDRESS:
106 ADDRESSEE: Pennie & Edmonds
107 STREET: 1155 Avenue of the Americas
108 CITY: New York
109 STATE: New York
110 COUNTRY: USA
111 ZIP: 10036-2711
112 COMPUTER READABLE FORM:
113 MEDIUM TYPE: Floppy disk
114 COMPUTER: IBM PC compatible
115 OPERATING SYSTEM: PC-DOS/MS-DOS
116 SOFTWARE: PatentIn Release #1.0, Version #1.30
117 CURRENT APPLICATION DATA:
118 APPLICATION NUMBER: US/08/486,099
119 FILING DATE: 07-JUN-1995
120 CLASSIFICATION: 435
121 ATTORNEY/AGENT INFORMATION:
122 NAME: Coruzzi, Laura A.
123 REGISTRATION NUMBER: 30,742
124 REFERENCE/DOCKET NUMBER: 7872-031
125 TELECOMMUNICATION INFORMATION:
126 TELEPHONE: (212) 790-9090
127 TELEFAX: (212) 869-9741/8864
128 TELEX: 66141 PENNIE
129 INFORMATION FOR SEQ ID NO: 107:
130 SEQUENCE CHARACTERISTICS:
131 LENGTH: 192 amino acids
132 TYPE: amino acid
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134 TOPOLOGY: unknown
135 MOLECULE TYPE: protein
136 US-08-486-099-107
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138 Query Match 2.1%; Score 7; DB 3; Length 192;
139 Best Local Similarity 100.0%; Pred. No. 83;
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1 COUNTRY: USA
2 ZIP: 20850
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6 OPERATING SYSTEM: PC-DOS/MS-DOS
7 SOFTWARE: PatentIn Release #1.0, Version #1.30
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/09/717,209
10 FILING DATE:
11 CLASSIFICATION:
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US/08/613,822
14 FILING DATE: 23-FEB-1996
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Millstein, Larry S
17 REGISTRATION NUMBER: 34,679
18 TELEPHONE: 301-309-8504
19 TELEFAX: 301-309-8512
20 INFORMATION FOR SEQ ID NO: 4:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 98 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: protein
26 US-09-717-209-4
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28 Query Match 2.1%; Score 7; DB 4; Length 98;
29 Best Local Similarity 100.0%; Pred. No. 46;
30 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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32 QY 227 VLLCILL 233
33 Db 6 VLLCILL 12
34
35 RESULT 14
36 US-08-486-099-107
37 Sequence 107, Application US/08486099
38 Patent No. 6013263
39 GENERAL INFORMATION:
40 APPLICANT: Bolognesi, Dani P.
41 APPLICANT: Matthews, Thomas J.
42 APPLICANT: Wild, Carl T.
43 APPLICANT: Barney, Shawn O.
44 APPLICANT: Lambert, Dennis M.
45 APPLICANT: Petteway, Stephen R.
46 APPLICANT: Langlois, Alphonse J.
47 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
48 TITLE OF INVENTION: B VIRUS TRANSMISSION
49 NUMBER OF SEQUENCES: 209
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: Pennie & Edmonds
52 STREET: 1155 Avenue of the Americas
53 CITY: New York
54 STATE: New York
55 COUNTRY: USA
56 ZIP: 10036-2711
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: PatentIn Release #1.0, Version #1.30
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/08/486,099
64 FILING DATE: 07-JUN-1995
65 CLASSIFICATION: 435
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Coruzzi, Laura A.
68 REGISTRATION NUMBER: 30,742
69 REFERENCE/DOCKET NUMBER: 7872-031
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: (212) 790-9090
72 TELEFAX: (212) 869-9741/8864
73 TELEX: 66141 PENNIE
74 INFORMATION FOR SEQ ID NO: 107:
75 SEQUENCE CHARACTERISTICS:
76 LENGTH: 192 amino acids
77 TYPE: amino acid
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79 TOPOLOGY: unknown
80 MOLECULE TYPE: protein
81 US-08-486-099-107
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84 Best Local Similarity 100.0%; Pred. No. 83;
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; Sequence 117, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-117

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Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Perfect score: 335

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	PRIOR APPLICATION NUMBER: 60/075945
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7	PRIOR APPLICATION NUMBER: 60/090695	
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7	PRIOR FILING DATE: 1998-06-26	
7	PRIOR APPLICATION NUMBER: 60/090863	
7	PRIOR FILING DATE: 1998-06-26	

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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305; Mismatches 0; Indels 0; Gaps 0;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLQLTGSAAGPVKELVGSVGGAVTFPLKSKVKQVDSIYVTFNTTPL 60
DB 1 MAGSPTCLTLIYLQLTGSAAGPVKELVGSVGGAVTFPLKSKVKQVDSIYVTFNTTPL 60

QY 61 VTIOEGGGTIIYTONRRNRVDFPDGGYSLKLSKLKNDGSIYVYGIYSSSLOQPSIOEY 120
DB 61 VTIOEGGGTIIYTONRRNRVDFPDGGYSLKLSKLKNDGSIYVYGIYSSSLOQPSIOEY 120

QY 121 VLHVYHLSKPKVTWGLQSKNGTCTVNLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180
DB 121 VLHVYHLSKPKVTWGLQSKNGTCTVNLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180

QY 181 PISWRGESDMTFCIVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLLVPLLSSL 240
DB 181 PISWRGESDMTFCIVARNPVSRNFSPIIARKLCEGAADDPSSMVLCLLLVPLLSSL 240

QY 241 FVLGLFWLFLKBEROEYIEEKRVDCIETNIPCHSGENTYDTIPIHTNRTILKEDPA 300
DB 241 FVLGLFWLFLKBEROEYIEEKRVDCIETNIPCHSGENTYDTIPIHTNRTILKEDPA 300

QY 301 NTVYSTVEIPKKWENPHSLTTPDTPRLFAYENVI 335
DB 301 NTVYSTVEIPKKWENPHSLTTPDTPRLFAYENVI 335

RESULT 3
US-09-989-723-253.
Sequence 253, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTPL 60
Db 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIWTNTTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGVYSSSIQQSTQRY 120
Db 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGVYSSSIQQSTQRY 120
QY 121 VLHVYHLSKPKVMTGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALGOANESHNGSL 180
Db 121 VLHVYHLSKPKVMTGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALGOANESHNGSL 180
QY 181 PISWRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSNMVLLCLLLVPLLSL 240
Db 181 PISWRWGESDMTFCVARNPVSRNPFSSPILARKLCEGAADDPDSNMVLLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKREOREEYIEKKRVDIICRETPNICPHSGENTEXTIPIHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREOREEYIEKKRVDIICRETPNICPHSGENTEXTIPIHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKQENPHSLTTPDTFRLPAYENVI 335
Db 301 NTVYSTVEIPKKQENPHSLTTPDTFRLPAYENVI 335

RESULT 4

US-09-989-279-253
; Sequence 253; Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

APPLICANT: Gerber,Hanspeter
APPLICANT: Gerritsen,Mary E.
APPLICANT: Goddard,Audrey
APPLICANT: Godowski,Paul J.
APPLICANT: Grimaldi,J.Christopher
APPLICANT: Gurney,Austin L.
APPLICANT: Kljavin,Ivar J.
APPLICANT: Napier,Mary A.
APPLICANT: Pan,James
APPLICANT: Paoni,Nicholas F.
APPLICANT: Roy,Margaret Ann
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K.
APPLICANT: Williams,P. Mickey
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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;; PRIOR FILING DATE: 1998-07-07
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 1.3e-305; Mismatches 0; Indels 0; Gaps 0;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 121 VLHVYHLSPKVTVMGLQKNKGTCTVNTLTCMEHGEEDVIYTWKALGOAANESHNGSL 180
Qy 181 PISWRGESDMTIFICVARNPVRNFSPIILARKLCEGAADDPDSSNVLLCLLIVPLLSSL 240
Db 181 PISWRGESDMTIFICVARNPVRNFSPIILARKLCEGAADDPDSSNVLLCLLIVPLLSSL 240
Qy 241 FVLGLFWLFLKREQBEYTEEKRVVDICRETNPICPHSGENTYDTIPTNRTILKEDPA 300
Db 241 FVLGLFWLFLKREQBEYTEEKRVVDICRETNPICPHSGENTYDTIPTNRTILKEDPA 300
Qy 301 NTVYSTVEIPKKNPHSLTTPDTPRLFAYENVI 335
Db 301 NTVYSTVEIPKKNPHSLTTPDTPRLFAYENVI 335

RESULT 5
US-09-989-727-253
; Sequence 253, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04

;	PRIOR FILING DATE:	1998-06-23	
;	PRIOR APPLICATION NUMBER:	60/090355	
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;	PRIOR APPLICATION NUMBER:	60/091626	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091633	
;	PRIOR FILING DATE:	1998-07-02	
;	PRIOR APPLICATION NUMBER:	60/091978	
;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/091982	
;	PRIOR FILING DATE:	1998-07-07	
;	PRIOR APPLICATION NUMBER:	60/092182	
;	PRIOR FILING DATE:	1998-07-09	

Query Match 100.0%; Score 335; DB 9; Length 335;

QY 181 PISWRGSDMTFICVARNPVSRNFSSPILARKLCEGAADDPSSWVLLCLLVPLLSSL 240
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
Db 181 PISWRGSDMTFICVARNPVSRNFSSPILARKLCEGAADDPSSWVLLCLLVPLLSSL 240
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
QY 241 FVLGLFLWFLKREOBEYEIEKKRVDICRETNPICPHSGENTYDTIPTHNRITLKEDPA 300
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
Db 241 FVLGLFLWFLKREOBEYEIEKKRVDICRETNPICPHSGENTYDTIPTHNRITLKEDPA 300
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
QY 301 NTYVSTVEIPKKMNPBSLTTMPDTPRLPAYENVI 335
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
Db 301 NTYVSTVEIPKKMNPBSLTTMPDTPRLPAYENVI 335
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18

RESULT 6
US-09-989-731-253
Sequence 253, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Faoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759

;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
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;; PRIOR APPLICATION NUMBER: 60/089952
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGSPTCLTIYILWOLTGSAASGPVKELVSGVGAATFPLKSKVKQVDSIVTWTNTPL 60
DB 1 MAGSPTCLTIYILWOLTGSAASGPVKELVSGVGAATFPLKSKVKQVDSIVTWTNTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDVDPDGGYSLKSLKNDGSIYVYVGIYSSSIQQPSTQBY 120
DB 61 VTIOPEGGTIIVTQNRNRVDVDPDGGYSLKSLKNDGSIYVYVGIYSSSIQQPSTQBY 120
QY 121 VLHVYHLSKPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSL 180
DB 121 VLHVYHLSKPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSL 180
QY 181 PISRWGESDMTFCVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCILLVPLLSL 240
DB 181 PISRWGESDMTFCVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCILLVPLLSL 240
QY 241 FVLGLFLWFLKREOEYIEBKRVDICRETPNICPHSGENTYDTIPTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEBKRVDICRETPNICPHSGENTYDTIPTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKNPHSLTMTPTPRLFAYENVI 335
DB 301 NTVYSTVEIPKKNPHSLTMTPTPRLFAYENVI 335

RESULT 7

US-09-989-732-253
; Sequence 253, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: ROY, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25

;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWQLTSAASGVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPCTCLTIYILWQLTSAASGVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
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DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDSDGIYVGYSSSLQQPSTQY 120
QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALQQAANESHGSI 180
DB 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALQQAANESHGSI 180
QY 181 PISRWGESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
DB 181 PISRWGESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAYENVI 335
DB 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAYENVI 335

RESULT 8
US-09-745-605-4
; Sequence 4, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
; APPLICANT: Starling, Gary C.
; APPLICANT: Finger, Joshua N.
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
; AND APEX-3 AND USES THEREOF
; FILE REFERENCE: DB13NP
; CURRENT APPLICATION NUMBER: US/09/745,605
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/172,025
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-745-605-4

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGSPCTCLTIYILWQLTSAASGVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDSDGIYVGYSSSLQQPSTQY 120
DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDSDGIYVGYSSSLQQPSTQY 120

QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALQQAANESHGSI 180
DB 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALQQAANESHGSI 180
QY 181 PISRWGESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
DB 181 PISRWGESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAYENVI 335
DB 301 NTVYSTVEIPKKNPHSLTMPDTPRLFAYENVI 335

RESULT 9
US-09-991-073-253
; Sequence 253, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; ACIDS
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
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; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607

PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182

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; PRIOR FILING DATE: 1998-07-09
Query Match      100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGSPCTCLTLYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60

QY 61 VTIOPEGGTTIIVQNRNRERVDFFDGGYSLKSLKNDSGIYYVGYSSLSLOQPSTOEY 120
DB 61 VTIOPEGGTTIIVQNRNRERVDFFDGGYSLKSLKNDSGIYYVGYSSLSLOQPSTOEY 120

QY 121 VLVYVHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVITYWKALQQAANESHNGSIL 180
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QY 181 PISRWGSDMTFFICVARNPVSRRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240
DB 181 PISRWGSDMTFFICVARNPVSRRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240

QY 241 FVLGLFWLFLKREQEYIEKKRVDIKRETPNICPHSGENTYDTIPTNRTILKEDPA 300
DB 241 FVLGLFWLFLKREQEYIEKKRVDIKRETPNICPHSGENTYDTIPTNRTILKEDPA 300

QY 301 NTVYSTVEIPKXWENPHSLTTPDTPRLFAYENV 335
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RESULT 10
US-09-990-442-253
; Sequence 253, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305; Indels 0; Gaps 0;
Matches 335; Conservative 0; Mismatches 0;

Qy 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVGAATFPLKSKVKQVDSIWTFTTTL 60
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Db 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYGIYSSSIQOQSTQBY 120

Qy 121 VLHVYEHLSKPKVTMGLOSKNKGTCVTNLTCCMEHGBEDVIYTWKALGQAANESHGSL 180
Db 121 VLHVYEHLSKPKVTMGLOSKNKGTCVTNLTCCMEHGBEDVIYTWKALGQAANESHGSL 180

Qy 181 PISWRWGESDMTFFICVARNPVSRNFPSSPILARKLCEGAADPPDSSMVLCLLLVPLLJSL 240
Db 181 PISWRWGESDMTFFICVARNPVSRNFPSSPILARKLCEGAADPPDSSMVLCLLLVPLLJSL 240

Qy 241 FVLGLFLWFLKRRQEEYIEBKRVDIQRETNPCPHSGENTYDTIPIHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKRRQEEYIEBKRVDIQRETNPCPHSGENTYDTIPIHTNRTILKEDPA 300

Qy 301 NTVYSTVEIPKKNPHSLTMDPTPLFAYENVI 335
Db 301 NTVYSTVEIPKKNPHSLTMDPTPLFAYENVI 335

RESULT 11
US-09-991-163-253
; Sequence 253, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC17
;; CURRENT APPLICATION NUMBER: US/09/991,163
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWOLTSAGSPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTTL 60
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QY 121 VLHVYHLKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL 180
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QY 181 PISWRGSDMTFICVARNPVSRNFSFSPILARKLCEGAADDPDSSNVLLCLLLVPLLISL 240
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QY 241 FVLGLFWLFLKRRQBEYIEEKRVVDICRETNICPHSGENTYDTPHTNRTILKEDPA 300
DB 241 FVLGLFWLFLKRRQBEYIEEKRVVDICRETNICPHSGENTYDTPHTNRTILKEDPA 300

QY 301 NTVYSTVEIPKKNENPHSLLTWPDTPRLFAYENVI 335
DB 301 NTVYSTVEIPKKNENPHSLLTWPDTPRLFAYENVI 335

RESULT 12
US-09-993-604-253
; Sequence 253, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Zhang, Zemin
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; FILE REFERENCE: P2730PIC25
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; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.3e-305;
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Qy 61 VTIQEGGTIIVTQNRNRVDPDGGYSLKSLKKNDSGIYVYSSLSQOPSTQY 120
Db 61 VTIQEGGTIIVTQNRNRVDPDGGYSLKSLKKNDSGIYVYSSLSQOPSTQY 120
Qy 121 VLHVYHLSKPKVTMGLOSNKNGTCVTNLTCCMEHGEDVIYTWKALGOAANESHGSL 180
Db 121 VLHVYHLSKPKVTMGLOSNKNGTCVTNLTCCMEHGEDVIYTWKALGOAANESHGSL 180
Qy 181 PISWRGESDMTFFICVARNPVSRNFSFILARKLCEGAADPDSSMWLLCLLLVPLLSL 240
Db 181 PISWRGESDMTFFICVARNPVSRNFSFILARKLCEGAADPDSSMWLLCLLLVPLLSL 240
Qy 241 FVLGLFLWFLKREQEEYIEEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREQEEYIEEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA 300
Qy 301 NTVYSTVEIPKKNPHSLTTPDTPRLFAYENVI 335
Db 301 NTVYSTVEIPKKNPHSLTTPDTPRLFAYENVI 335

RESULT 13
US-09-990-456-253
; Sequence 253, Application US/09990456

Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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DB 61 VTIOPEGGTIIIVTQNNRERVDPPGGYSLKSLKNDGSGYVYVYSSSIQQPSTOEY 120

QY 121 VLHVYHLSKPKVTMGLQSNKNGTCVTNLTCCMERGEEDVITYTKALQGAANESHSIL 180
DB 121 VLHVYHLSKPKVTMGLQSNKNGTCVTNLTCCMERGEEDVITYTKALQGAANESHSIL 180

QY 181 PISRWGESDMTIFICVARNPVSRSNFPSPILARKLCEGAADPDSSMWLLCLLLVPLLSL 240
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QY 241 FVLGLFWLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
DB 241 FVLGLFWLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300

QY 301 NTVSTVTEIPKKMENPHSLTTPDTTPRLFAYENVI 335
DB 301 NTVSTVTEIPKKMENPHSLTTPDTTPRLFAYENVI 335

RESULT 14
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; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 335; DB 9; Length 335;
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Db 61 VTIOPEGGIIYVTONRNRVDPDGGYSLKSLKKNDSGIYVGIYSSSLOOQSTQBY 120
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QY 181 PISWRGSDMTFICVARNPVRNFSSPILARKLCEGAADDPDSNVLCLLLVPLLSSL 240
Db 181 PISWRGSDMTFICVARNPVRNFSSPILARKLCEGAADDPDSNVLCLLLVPLLSSL 240
QY 241 FVLGLFWLFLKEROEYIEEKRVVDICRETNI CPHSGENTYDTIPTHTNRTILKEDPA 300
Db 241 FVLGLFWLFLKEROEYIEEKRVVDICRETNI CPHSGENTYDTIPTHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKKMENPHSLTTPDTPRLPAYENVI 335
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RESULT 15
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; Sequence 253, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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64	PRIOR APPLICATION NUMBER: 60/091519	
65	PRIOR FILING DATE: 1998-07-02	
66	PRIOR APPLICATION NUMBER: 60/091478	
67	PRIOR FILING DATE: 1998-07-02	
68	PRIOR APPLICATION NUMBER: 60/091544	
69	PRIOR FILING DATE: 1998-07-01	
70	PRIOR APPLICATION NUMBER: 60/091519	
71	PRIOR FILING DATE: 1998-07-02	
72	PRIOR APPLICATION NUMBER: 60/091626	
73	PRIOR FILING DATE: 1998-07-02	
74	PRIOR APPLICATION NUMBER: 60/091633	
75	PRIOR FILING DATE: 1998-07-02	

[illegible]

Search completed: August 18, 2004, 15:58:09
Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:57:14 ; Search time 16 Seconds
(without alignments)
2014.010 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335

Sequence: 1 MAGSPTCLTYILWQLTGS.....PHSLLTMPDTPRLPAYENVI 335

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : PIR 78:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	8	2.4	705	2	glutenin high mole
6	8	2.4	1117	2	desmoglein 2 - hum
7	7	2.1	105	2	hypothetical prote
8	7	2.1	161	2	hypothetical prote
9	7	2.1	170	2	hypothetical prote
10	7	2.1	179	2	ribosomal protein
11	7	2.1	179	2	hypothetical prote
12	7	2.1	182	2	hypothetical prote
13	7	2.1	184	2	hypothetical prote
14	7	2.1	189	2	hypothetical prote
15	7	2.1	199	2	hypothetical prote
16	7	2.1	220	2	hypothetical prote
17	7	2.1	228	2	hypothetical prote
18	7	2.1	238	2	hypothetical prote
19	7	2.1	238	2	conserved hypothet
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21	7	2.1	239	2	hypothetical prote
22	7	2.1	266	2	flagellar biosynth
23	7	2.1	274	2	cysteine synthase
24	7	2.1	290	2	protein T25C8.3 li
25	7	2.1	301	2	probable thiosulfa
26	7	2.1	301	2	UDP-N-acetylenolpy
27	7	2.1	302	2	PecM-related prote
28	7	2.1	303	2	UDP-N-acetylenolpy
29	7	2.1	305	2	UDP-N-acetylenolpy

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34	7	2.1	348	2	E84299
35	7	2.1	351	2	C82755
36	7	2.1	356	2	S14396
37	7	2.1	362	2	S68471
38	7	2.1	367	2	S41024
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87	7	2.1	959	2	AB0111
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89	7	2.1	1002	2	S62035
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91	7	2.1	1032	2	S53571
92	7	2.1	1070	2	T06733
93	7	2.1	1085	2	S55352
94	7	2.1	1166	2	T15628
95	7	2.1	1268	2	A49674
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101	7	2.1	1355	2	T22552
102	7	2.1	1487	2	S15904

apolipoprotein E P
UDP-N-acetylenolpy
protein F07G6.1 li
hypothetical prote
conserved hypothet
cytochrome-c oxida
asparaginase (EC 3
hypothetical prote
hypothetical prote
protein C18B12.2 l
cycH protein - Rhi
ubiquinol-cytochro
poly(A) polymerase
hypothetical prote
tryptophan transpo
membrane transport
probable membrane
conserved hypothet
gluconate permease
hypothetical prote
efflux pump antibi
conserved hypothet
beta-glucosidase h
beta-glucosidase h
hypothetical prote
hypothetical prote
tolerance to colic
sensor histidine k
probable ABC trans
probable thioredox
DNA damage-inducib
cytochrome-c oxida
env polyprotein -
env polyprotein -
calnexin precursor
calnexin precursor
copper resistance
hypothetical prote
conserved hypothet
hypothetical prote
NADH2 dehydrogenas
acylaminoacyl-pept
hypothetical prote
probable cell divi
probable helicase
penicillin-binding
excinuclease ABC, c
excinuclease ABC c
glycine cleavage s
glycine cleavage s
glycine decarboxyl
hypothetical prote
glycine dehydrogen
glycine dehydrogen
glycine cleavage s
glycine dehydrogen
hypothetical prote
isoleucine-tRNA li
glycine dehydrogen
hypothetical prote
kinesin homolog F2
IFH1 protein - ysa
hypothetical prote
flightless-I homol
hypothetical prote
period protein hom
DNA-directed DNA p
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hypothetical prote
alpha-1 proteinase

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105	7	2.1	1585	2	A92916	NAD-glutamate dehy	178	6	1.8	111	2	B83101	hypothetical prote
106	7	2.1	1585	2	H97690	NAD-glutamate dehy	179	6	1.8	112	2	S48472	probable membrane
107	7	2.1	1620	2	S61535	nucleotide-binding	180	6	1.8	113	2	S26266	T-cell receptor be
108	7	2.1	2787	2	S45416	TEU1 protein - yea	181	6	1.8	113	2	S17385	T-cell receptor be
109	7	2.1	3973	2	B71612	hypothetical prote	182	6	1.8	113	2	S26262	T-cell receptor be
110	7	2.1	4545	1	S25111	alpha-2-macroglobu	183	6	1.8	113	2	S26263	T-cell receptor be
111	6	1.8	30	2	I57689	ubiquinol-cytochro	184	6	1.8	113	2	JC4143	molt-inhibiting ho
112	6	1.8	32	2	S21547	T-cell receptor al	185	6	1.8	113	2	AD2868	hypothetical prote
113	6	1.8	36	2	H64607	hypothetical prote	186	6	1.8	113	2	AC3033	hypothetical prote
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138	6	1.8	96	2	B64076	chaperonin groES -	211	6	1.8	129	2	F95987	conserved hypothe
139	6	1.8	96	2	C82048	chaperonin, 10 kD	212	6	1.8	132	2	C87431	hypothetical prote
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143	6	1.8	97	2	JC5770	chaperonin groES-1	216	6	1.8	133	2	C36886	hypothetical prote
144	6	1.8	97	2	A86110	chaperonin mopB [s	217	6	1.8	134	2	D87021	probable DNA-bind
145	6	1.8	97	2	A13269	chaperonin groES [218	6	1.8	135	2	A70659	hypothetical prote
146	6	1.8	97	2	AD1045	GroES protein [imp	219	6	1.8	135	2	B83440	hypothetical prote
147	6	1.8	97	2	E97266	glu-tRNA amidotran	220	6	1.8	135	2	F87156	hypothetical prote
148	6	1.8	98	2	S41828	NADH2 dehydrogenas	221	6	1.8	136	2	AD0650	probable exported
149	6	1.8	98	2	S4920	NADH2 dehydrogenas	222	6	1.8	136	2	T22797	hypothetical prote
150	6	1.8	98	2	T11488	NADH2 dehydrogenas	223	6	1.8	137	1	F64961	hypothetical prote
151	6	1.8	99	1	A39296	monocyte chemoatr	224	6	1.8	137	2	S03489	T-cell receptor be
152	6	1.8	99	2	JC5295	monocyte chemoatr	225	6	1.8	137	2	C85815	hypothetical prote
153	6	1.8	99	2	JC2336	monocyte chemoatr	226	6	1.8	137	2	D90967	hypothetical prote
154	6	1.8	99	2	JC2136	monocyte chemoatr	227	6	1.8	137	2	A44031	probable membrane
155	6	1.8	99	2	A02999	monocyte chemoatr	228	6	1.8	139	2	S36296	T-cell receptor ga
156	6	1.8	99	2	JC2417	monocyte chemoatr	229	6	1.8	140	2	C81176	hypothetical prote
157	6	1.8	100	2	E49999	NADH2 dehydrogenas	230	6	1.8	140	2	A99253	hypothetical prote
158	6	1.8	100	2	C91024	NADH dehydrogenase	231	6	1.8	141	2	E32998	chorion protein S1
159	6	1.8	100	2	D85868	NADH dehydrogenase	232	6	1.8	141	2	D81309	probable acetyltra
160	6	1.8	100	2	A03110	NADH2 dehydrogenas	233	6	1.8	142	2	T27965	hypothetical prote
161	6	1.8	100	2	A07996	NADH2 dehydrogenas	234	6	1.8	143	2	D75617	response regulator
162	6	1.8	100	2	E69846	hypothetical prote	235	6	1.8	144	2	T27945	hypothetical prote
163	6	1.8	101	2	S37068	NADH2 dehydrogenas	236	6	1.8	145	2	G82617	VirK protein XP194
164	6	1.8	101	2	S64222	probable membrane	237	6	1.8	146	2	S26408	T-cell receptor be
165	6	1.8	102	2	F87993	protein ZC334.3 [i	238	6	1.8	146	2	T45385	ribosomal protein
166	6	1.8	103	2	B27692	probable membrane	239	6	1.8	146	2	T27964	hypothetical prote
167	6	1.8	106	2	S97734	hypothetical prote	240	6	1.8	149	2	AD3431	hypothetical prote
168	6	1.8	107	2	PH0987	ig heavy chain V r	241	6	1.8	150	2	S43955	probable NADH2 deh
169	6	1.8	107	2	C70188	hypothetical prote	242	6	1.8	150	2	A87714	hypothetical prote
170	6	1.8	108	2	S73125	hypothetical prote	243	6	1.8	151	2	S48958	hypothetical prote
171	6	1.8	108	2	A55590	hypothetical prote	244	6	1.8	151	2	A83784	acetyltransferase
172	6	1.8	108	2	I40598	hypothetical prote	245	6	1.8	152	2	S21826	T-cell receptor be
173	6	1.8	109	2	A54678	monocyte chemoatr	246	6	1.8	152	2	F66318	protein F15H18.2 [
174	6	1.8	109	2	H71142	hypothetical prote	247	6	1.8	153	1	A28406	gastric inhibitory
175	6	1.8	111	2	G75009	hypothetical prote	248	6	1.8	153	2	C64373	hypothetical prote

249	6	1.8	153	2	E87306	hypothetical prote	322	6	1.8	205	2	S42406	protein phosphatas
250	6	1.8	157	2	S57451	cysteine proteinas	323	6	1.8	206	2	S10497	hypothetical prote
251	6	1.8	157	2	T24917	hypothetical prote	324	6	1.8	205	2	AE0891	probable membrane
252	6	1.8	158	2	H96900	probable HD superf	325	6	1.8	206	2	S61705	hypothetical prote
253	6	1.8	159	2	D90586	hypothetical prote	326	6	1.8	206	2	A82222	hypothetical prote
254	6	1.8	161	2	E72339	hypothetical prote	327	6	1.8	207	2	A35535	23K calcium-bindin
255	6	1.8	162	1	CFPKA	C-phycocyanin alph	328	6	1.8	209	2	H69552	hypothetical prote
256	6	1.8	162	1	CFMWA	C-phycocyanin alph	329	6	1.8	209	2	S69926	outer surface prot
257	6	1.8	162	2	S30940	phycocyanin alpha	330	6	1.8	209	2	I40285	outer surface prot
258	6	1.8	162	2	H72351	hypothetical prote	331	6	1.8	210	2	T50713	urease accessory p
259	6	1.8	163	2	A29674	phycocyanin alpha	332	6	1.8	210	2	G97037	hypothetical prote
260	6	1.8	163	2	AH1872	phycocyanin alpha	333	6	1.8	211	2	S69932	outer surface prot
261	6	1.8	165	2	G82910	peptide methionine	334	6	1.8	211	2	C59091	hypothetical prote
262	6	1.8	166	2	T11099	NADH2 dehydrogenas	335	6	1.8	212	2	B29010	alkylmercury lyase
263	6	1.8	170	2	T30570	hypothetical prote	336	6	1.8	212	2	S69921	outer surface prot
264	6	1.8	171	2	E75562	MutT/mudix family	337	6	1.8	212	2	S20543	outer surface prot
265	6	1.8	171	2	H87440	hypothetical prote	338	6	1.8	213	2	S74247	CDP diacylglycerol
266	6	1.8	172	1	DERTN6	NADH2 dehydrogenas	339	6	1.8	213	2	S07573	amine oxidase (fla
267	6	1.8	172	2	H72077	ct006 hypothetical	340	6	1.8	213	2	C70346	UDP-N-acetoenolpyr
268	6	1.8	172	2	C81590	conserved hypothet	341	6	1.8	214	1	S18729	adenyl-1-sulfate k
269	6	1.8	172	2	H86545	CT006 hypothetical	342	6	1.8	214	2	T21585	hypothetical prote
270	6	1.8	174	2	T01486	hypothetical prote	343	6	1.8	215	2	G95170	hemolysin limorte
271	6	1.8	176	2	S35949	edea protein - tre	344	6	1.8	215	2	G98036	conserved hypothet
272	6	1.8	176	2	JC6152	orphanin FQ precu	345	6	1.8	215	2	T87879	TFS1 related prote
273	6	1.8	177	2	S45364	ribosomal protein	346	6	1.8	216	2	H72277	hypothetical prote
274	6	1.8	177	2	B91248	hypothetical prote	347	6	1.8	216	2	T00192	hypothetical prote
275	6	1.8	178	2	S54190	outer surface prot	348	6	1.8	217	2	S65830	alpha fucosidase p
276	6	1.8	179	2	S36295	T-cell receptor ga	349	6	1.8	217	2	S49578	trypsin inhibitor
277	6	1.8	179	2	S54186	outer surface prot	350	6	1.8	217	2	H72390	dihydroorotate deh
278	6	1.8	179	2	S54187	outer surface prot	351	6	1.8	217	2	F91246	PTS system, sorbos
279	6	1.8	179	2	S54188	outer surface prot	352	6	1.8	218	2	B83862	endonuclease III (
280	6	1.8	179	2	T35439	probable integral	353	6	1.8	218	2	G64673	DNA polymerase III
281	6	1.8	180	2	S54189	outer surface prot	354	6	1.8	218	2	B71844	probable DNA poyme
282	6	1.8	180	2	S54191	outer surface prot	355	6	1.8	218	2	S74867	hypothetical prote
283	6	1.8	181	2	G89799	hypothetical prote	356	6	1.8	219	2	S49428	hypothetical prote
284	6	1.8	181	2	I40146	outer surface prot	357	6	1.8	221	1	S43328	glutathione peroxi
285	6	1.8	181	2	AC0686	hypothetical prote	358	6	1.8	221	2	A47367	24K androgen-depen
286	6	1.8	184	2	S73640	inorganic diphosph	359	6	1.8	221	2	B42719	O-methyltransferas
287	6	1.8	185	2	AG2026	hypothetical prote	360	6	1.8	222	2	JC7697	beta-casein-like p
288	6	1.8	186	1	HHFF23	heat shock protein	361	6	1.8	222	2	AD2999	thiol-disulfide in
289	6	1.8	186	2	T11384	ATPase subunit 6 -	362	6	1.8	222	2	E98284	thiol-disulfide in
290	6	1.8	186	2	B20647	heat shock protein	363	6	1.8	223	2	S94942	histone H1 - mouse
291	6	1.8	186	2	T47804	hypothetical prote	364	6	1.8	224	2	F69444	conserved hypothet
292	6	1.8	187	2	G95076	conserved hypothet	365	6	1.8	225	2	G70721	hypothetical prote
293	6	1.8	187	2	H70450	lipoprotein nlpd h	366	6	1.8	227	2	F97276	CPSP/CAPA conserve
294	6	1.8	188	2	S50158	RER1 protein - yea	367	6	1.8	227	2	D84775	hypothetical prote
295	6	1.8	188	2	A69880	hypothetical prote	368	6	1.8	228	2	B90369	hypothetical prote
296	6	1.8	190	2	T33366	hypothetical prote	369	6	1.8	229	2	B90534	trna/rna methyltr
297	6	1.8	191	2	F82430	periplasmic nitrat	370	6	1.8	229	2	T18629	hypothetical prote
298	6	1.8	191	2	S70262	outer surface prot	371	6	1.8	230	2	D84215	hypothetical prote
299	6	1.8	192	2	S22981	T-cell surface gly	372	6	1.8	230	2	T36263	probable transcrip
300	6	1.8	192	2	JC1663	T-cell receptor CD	373	6	1.8	231	2	A81798	probable N-acetyl
301	6	1.8	193	2	S70259	outer surface prot	374	6	1.8	232	2	B69392	ABC transporter, A
302	6	1.8	193	2	S70274	outer surface prot	375	6	1.8	233	2	B64525	trbi protein - Hel
303	6	1.8	193	2	S70286	outer surface prot	376	6	1.8	235	2	S48924	hypothetical prote
304	6	1.8	194	2	D97944	conserved hypothet	377	6	1.8	236	2	D84961	orotidine-5'-phosp
305	6	1.8	194	2	C83312	hypothetical prote	378	6	1.8	236	2	C75516	hypothetical prote
306	6	1.8	196	2	S54196	outer surface prot	379	6	1.8	236	2	E75337	hypothetical prote
307	6	1.8	197	2	E70642	probable ribosomal	380	6	1.8	237	2	S08073	cyclic nucleotide
308	6	1.8	197	2	C90671	hypothetical prote	381	6	1.8	237	2	S34727	listeriolysin regu
309	6	1.8	197	2	G85521	hypothetical prote	382	6	1.8	237	2	AH1424	a probable N-acety
310	6	1.8	197	2	B83768	hypothetical prote	383	6	1.8	237	2	T05249	hypothetical prote
311	6	1.8	200	2	E64756	membrane protein y	384	6	1.8	239	2	A81437	probable integral
312	6	1.8	200	2	A81295	probable membrane	385	6	1.8	239	2	T31881	hypothetical prote
313	6	1.8	201	2	D86912	conserved hypothet	386	6	1.8	240	2	AD1950	hypothetical prote
314	6	1.8	202	2	T10016	hypothetical prote	387	6	1.8	240	2	T47589	synaptobrevin-like
315	6	1.8	202	2	D69046	conserved hypothet	388	6	1.8	240	2	AG0048	hypothetical prote
316	6	1.8	202	2	B83375	hypothetical prote	389	6	1.8	241	2	T33804	hypothetical prote
317	6	1.8	203	2	AC0620	hypothetical proph	390	6	1.8	241	2	C86492	hypothetical prote
318	6	1.8	203	2	S32799	hypothetical prote	391	6	1.8	241	2	C72130	hypothetical prote
319	6	1.8	204	2	H70648	probable regulator	392	6	1.8	242	2	JC7517	1-5-phosphoribosy
320	6	1.8	204	2	T72370	hypothetical prote	393	6	1.8	243	2	G81255	ATPase chain 6 [im
321	6	1.8	204	2	T51012	hypothetical prote	394	6	1.8	244	2	T43764	

395	6	1.8	245	2	D36145	precorrin-2 methyl	468	6	1.8	276	2	A10565	lipoprotein [impor
396	6	1.8	245	2	B75340	transcription regu	469	6	1.8	276	2	E91117	hypothetical prote
397	6	1.8	245	2	F83105	hypothetical prote	470	6	1.8	276	2	F72342	conserved hypochet
398	6	1.8	246	2	T00704	hypothetical prote	471	6	1.8	276	2	T00923	hypothetical prote
399	6	1.8	247	2	A75254	conserved hypochet	472	6	1.8	276	2	JT0591	Au11 protein - yea
400	6	1.8	247	2	E86250	protein F25C20.16	473	6	1.8	277	2	T32460	hypothetical prote
401	6	1.8	247	2	S66064	conserved hypochet	474	6	1.8	277	2	B69479	conserved hypochet
402	6	1.8	248	2	D69094	phosphoribosylamin	475	6	1.8	278	1	TDRTOX	OX-2 membrane glyc
403	6	1.8	249	2	S23902	genome polypeptin	476	6	1.8	279	2	E75472	ROK family protein
404	6	1.8	249	2	C75156	hypothetical prote	477	6	1.8	280	2	T02004	chitinase [EC 3.2.
405	6	1.8	250	2	H83213	hypothetical prote	478	6	1.8	280	2	B81100	2-dehydro-3-deoxyp
406	6	1.8	250	2	T40977	cdp-diacylglycerol	479	6	1.8	280	2	G81840	2-dehydro-3-deoxy-
407	6	1.8	250	2	E82821	NADH-ubiquinone ox	480	6	1.8	280	2	B45537	viral coat protein
408	6	1.8	251	2	C84036	succinate dehydrog	481	6	1.8	280	2	T32747	hypothetical prote
409	6	1.8	251	2	AC2187	phospho-2-dehydro-	482	6	1.8	280	2	B87547	transcription regu
410	6	1.8	251	2	B64851	flagellar basal bo	483	6	1.8	281	1	D69030	Mu1235-related pro
411	6	1.8	251	2	G90810	flagellar rod prot	484	6	1.8	281	2	B47092	copy control prote
412	6	1.8	251	2	C85670	flagellar rod prot	485	6	1.8	281	2	B86820	conserved hypochet
413	6	1.8	251	2	E72578	hypothetical prote	486	6	1.8	282	1	SAVL64	middle surface ant
414	6	1.8	252	2	H90212	enoyl CoA hydratase	487	6	1.8	282	2	AC3084	shikimate 5-dehydr
415	6	1.8	252	2	B47188	MHC class II histo	488	6	1.8	283	2	AH0726	phosphotransferase
416	6	1.8	253	2	S05029	H+-transporting tw	489	6	1.8	283	2	AC1340	maltodextrin ABC-t
417	6	1.8	253	2	D88427	protein R07E5.15 [490	6	1.8	283	2	A11710	maltodextrin ABC-t
418	6	1.8	253	2	T130928	hypothetical prote	491	6	1.8	284	2	H64914	probable dimethyls
419	6	1.8	254	1	VCCVTV	coat protein - tob	492	6	1.8	284	2	H90915	probable DMSO redu
420	6	1.8	254	2	S25281	glTF protein precu	493	6	1.8	284	2	E85764	probable DMSO redu
421	6	1.8	255	2	F84244	proteasome, subuni	494	6	1.8	284	2	T72222	UDP-N-acetylenolpy
422	6	1.8	256	2	T22715	hypothetical prote	495	6	1.8	284	2	T36934	probable transport
423	6	1.8	256	2	T00165	repressor - Staphy	496	6	1.8	285	2	E81388	probable succinate
424	6	1.8	257	2	B70246	outer surface prot	497	6	1.8	285	2	C98105	hypothetical prote
425	6	1.8	257	2	AC0087	probable flagellar	498	6	1.8	285	2	B95241	conserved hypochet
426	6	1.8	259	1	ONCAOL	ovulation hormone	499	6	1.8	286	1	WQECMM	phosphotransferase
427	6	1.8	260	2	I51544	MHC class II beta-	500	6	1.8	286	2	A98945	mannose-specific p
428	6	1.8	260	2	I51542	MHC class II beta-	501	6	1.8	286	2	D85793	PTS enzyme IID, ma
429	6	1.8	260	2	T33869	hypothetical prote	502	6	1.8	286	2	H64053	murein endopeptida
430	6	1.8	260	2	T29909	hypothetical prote	503	6	1.8	287	1	A45168	probable 3-oxoacyl
431	6	1.8	260	2	S60480	low temperature-in	504	6	1.8	287	2	T04236	xyloglucan endo-1,
432	6	1.8	261	2	A33499	O-sialoglycoprotei	505	6	1.8	288	2	S36956	cytochrome-c oxida
433	6	1.8	261	2	S10321	31K protein - frog	506	6	1.8	288	2	S28029	gene PD-1 protein
434	6	1.8	261	2	D95271	hypothetical prote	507	6	1.8	288	2	S18438	sporulation protei
435	6	1.8	262	1	OTFF3	cytochrome-c oxida	508	6	1.8	289	1	S25286	probable dehydroge
436	6	1.8	262	2	A81504	conserved hypochet	509	6	1.8	289	2	T41305	hypothetical prote
437	6	1.8	262	2	B72037	CT598 hypochet	510	6	1.8	291	2	F98202	shikimate 5-dehydr
438	6	1.8	262	2	E86588	CT598 hypochet	511	6	1.8	293	2	S04649	beta-lactamase (EC
439	6	1.8	263	1	S23009	insulin-like growt	512	6	1.8	293	2	T09171	ribosomal protein'
440	6	1.8	263	2	E72675	hypothetical prote	513	6	1.8	293	2	T09170	ribosomal protein
441	6	1.8	263	2	C69064	conserved hypochet	514	6	1.8	293	2	A83623	hypothetical prote
442	6	1.8	264	2	H81720	conserved hypochet	515	6	1.8	295	2	E84336	sugar kinase limpo
443	6	1.8	265	2	S16592	chlorophyll a/b-bi	516	6	1.8	295	2	AC0214	PTS system, mannos
444	6	1.8	265	2	F69742	hypothetical prote	517	6	1.8	296	2	T45930	uracil phosphoribo
445	6	1.8	267	2	A86891	hypothetical prote	518	6	1.8	296	2	T00559	hypothetical prote
446	6	1.8	267	2	H82201	probable bax prote	519	6	1.8	296	2	A36966	probable dtp-p-rham
447	6	1.8	267	2	T29500	hypothetical prote	520	6	1.8	297	2	B91102	replication initi
448	6	1.8	267	2	C75131	hypothetical prote	521	6	1.8	297	2	F85947	replication initi
449	6	1.8	267	2	S70291	hypothetical prote	522	6	1.8	297	2	S22098	chromosome initi
450	6	1.8	268	2	A71086	hypothetical prote	523	6	1.8	297	2	AF0874	FluA17.4 [imported
451	6	1.8	269	2	A75397	probable signal pe	524	6	1.8	297	2	C96524	hypothetical prote
452	6	1.8	269	2	I51539	MHC class II beta-	525	6	1.8	297	2	F70572	hypothetical prote
453	6	1.8	269	2	I51540	MHC class II beta-	526	6	1.8	297	2	A70347	UNP-N-acetylenolpy
454	6	1.8	269	2	S73999	hypothetical prote	527	6	1.8	298	2	T36900	probable integral
455	6	1.8	269	2	T04095	ribonuclease S hom	528	6	1.8	298	2	B35272	osteoinductive fac
456	6	1.8	269	2	H98273	iron(III) dicitrat	529	6	1.8	298	2	T20841	hypothetical prote
457	6	1.8	270	2	I51543	MHC class II beta-	530	6	1.8	299	2	T04669	probable membrane
458	6	1.8	270	2	S57457	formylmethanofuran	531	6	1.8	299	2	AB0609	hypothetical prote
459	6	1.8	271	2	H83059	phosphatidylserine	532	6	1.8	299	2	T20953	proteinase IV homo
460	6	1.8	272	2	D87075	probable conserved	533	6	1.8	300	2	AB4220	spermidine synthas
461	6	1.8	273	2	B64446	formylmethanofuran	534	6	1.8	301	2	D90224	hypothetical prote
462	6	1.8	274	2	A47639	OX-2 membrane glyc	535	6	1.8	301	2	T37031	chromosome initiat
463	6	1.8	274	2	D97653	hypothetical prote	536	6	1.8	302	2	AE0112	conserved hypochet
464	6	1.8	274	2	AB2877	conserved hypochet	537	6	1.8	302	2	H87476	probable DNA-direc
465	6	1.8	275	2	S74417	hypothetical prote	538	6	1.8	303	2	T30737	ferrichrome-bindin
466	6	1.8	275	2	S03967	intercellular adhe	539	6	1.8	303	2	A10411	hypothetical prote
467	6	1.8	276	1	FWBAA	H+-transporting tw	540	6	1.8	303	2	S23440	hypothetical prote

541	6	1.8	304	2	T34271	hypothetical prote	614	6	1.8	338	2	AF3617	oligopeptide trans
542	6	1.8	304	2	A86614	UDP-N-acetylenolp	615	6	1.8	338	2	T49998	hypothetical prote
543	6	1.8	304	2	T40316	conserved kin7-lik	616	6	1.8	339	2	S08981	malate dehydrogena
544	6	1.8	304	2	E72010	udp-n-acetylenolp	617	6	1.8	339	2	S73840	ribonucleotide red
545	6	1.8	304	2	C81530	UDP-N-acetylenolp	618	6	1.8	340	2	C64225	ribonucleotide red
546	6	1.8	305	2	JN0647	hydrogenase expres	619	6	1.8	340	2	B66661	unknown protein, 8
547	6	1.8	305	2	T35344	probable oxidoredu	620	6	1.8	340	2	T22010	hypothetical prote
548	6	1.8	305	2	AF2843	conserved hypotet	621	6	1.8	341	2	S55627	hypothetical prote
549	6	1.8	305	2	G97620	hypothetical prote	622	6	1.8	341	2	C90579	hypothetical prote
550	6	1.8	305	2	D88656	protein F56D6.4 [i	623	6	1.8	342	2	S53663	hydrogenase-relate
551	6	1.8	305	2	C84189	hypothetical prote	624	6	1.8	342	2	E90772	periplasmic protei
552	6	1.8	306	2	F83348	probable transcrip	625	6	1.8	342	2	A56335	part of regulation
553	6	1.8	306	2	S77062	hypothetical prote	626	6	1.8	342	2	H64840	torf protein precu
554	6	1.8	307	2	B75120	phosphoglycerate d	627	6	1.8	343	2	A84335	chloromuconate cyc
555	6	1.8	307	2	E71011	probable phosphogl	628	6	1.8	343	2	AC3403	general L-amino ac
556	6	1.8	307	2	C81862	conserved hypotet	629	6	1.8	344	2	E84376	Na+/Ca2+-exchangin
557	6	1.8	307	2	D81082	conserved hypotet	630	6	1.8	344	2	T34981	probable integral
558	6	1.8	308	1	CRU06	carbonate dehydrat	631	6	1.8	345	2	S28140	gas vesicle protei
559	6	1.8	308	2	AG3317	zinc dehydrogenase (E	632	6	1.8	345	2	A82251	hypothetical prote
560	6	1.8	309	2	H75113	NADH2 dehydrogenas	633	6	1.8	345	2	AB3035	conserved hypotet
561	6	1.8	309	2	H89832	hypothetical prote	634	6	1.8	347	2	T11338	NADH2 dehydrogenas
562	6	1.8	310	2	T40802	conserved hypotet	635	6	1.8	347	2	T11481	probable 3-hydroxy
563	6	1.8	311	2	S39661	menaquinone biosyn	636	6	1.8	347	2	B75610	tsec-1 protein (A
564	6	1.8	311	2	E95178	inorganic pyrophos	637	6	1.8	347	2	JC5788	probable ABC trans
565	6	1.8	311	2	D98045	manganese-dependen	638	6	1.8	349	2	H95421	conserved hypotet
566	6	1.8	311	2	AH3197	transmembrane sens	639	6	1.8	350	2	B82777	REIC protein - hum
567	6	1.8	312	2	G84058	cysteine synthase	640	6	1.8	350	2	JC7188	heat shock transcr
568	6	1.8	312	2	H89884	hypothetical prote	641	6	1.8	351	2	S25480	spindle body prote
569	6	1.8	313	2	T09670	abscisic acid acti	642	6	1.8	351	2	JQ2166	wnt-2 protein - fr
570	6	1.8	313	2	AB3186	transcription regu	643	6	1.8	352	2	S24559	matrix protein - H
571	6	1.8	313	2	H84169	hypothetical prote	644	6	1.8	352	2	T08209	Ribonuclease III r
572	6	1.8	315	2	T37901	probable purine nu	645	6	1.8	352	2	T49432	L-iditol 2-dehydro
573	6	1.8	315	2	JC5836	olfactory receptor	646	6	1.8	353	1	A45052	hypothetical prote
574	6	1.8	317	2	F82362	hydroxymethylbilan	647	6	1.8	353	2	A87643	probable UDP-N-ace
575	6	1.8	317	2	B83039	probable permease	648	6	1.8	354	2	C71368	hypothetical prote
576	6	1.8	317	2	D89961	conserved hypotet	649	6	1.8	354	2	A90012	phosphate starvat
577	6	1.8	317	2	T21046	hypothetical prote	650	6	1.8	354	2	B47065	hypothetical prote
578	6	1.8	319	2	A95282	ABC transporter, p	651	6	1.8	354	2	B85647	hypothetical prote
579	6	1.8	319	2	S44746	CO4D8.1 protein -	652	6	1.8	354	2	B90787	ATP-binding pho re
580	6	1.8	323	2	AE0324	probable membrane	653	6	1.8	354	2	T22274	hypothetical prote
581	6	1.8	324	2	A69648	2-keto-3-deoxygluc	654	6	1.8	355	1	S22181	gamma-1-microglobu
582	6	1.8	324	2	B66606	probable nicotiana	655	6	1.8	355	2	T03785	L-lactate dehydrog
583	6	1.8	326	2	PRW0JA	proteinase (EC 3.4	656	6	1.8	356	2	C70249	hypothetical prote
584	6	1.8	327	2	G70402	conserved hypotet	657	6	1.8	356	2	S58529	alpha-complex prot
585	6	1.8	328	2	A70871	probable quinone o	658	6	1.8	356	2	JQ2352	glycoprotein I - t
586	6	1.8	328	2	B84545	hypothetical prote	659	6	1.8	357	2	AD3491	hypothetical membr
587	6	1.8	328	2	D69452	conserved hypotet	660	6	1.8	358	2	D99823	hypothetical prote
588	6	1.8	328	2	C69358	reductase homolog	661	6	1.8	359	2	H95892	probable oxidoredu
589	6	1.8	328	2	D72566	hypothetical prote	662	6	1.8	359	2	D83385	hypothetical prote
590	6	1.8	328	2	S57128	hypothetical prote	663	6	1.8	359	2	T26813	hypothetical prote
591	6	1.8	329	2	T10203	hypothetical prote	664	6	1.8	359	2	G86290	hypothetical prote
592	6	1.8	329	2	H71192	hypothetical prote	665	6	1.8	359	2	AH3465	oxidoreductase (EC
593	6	1.8	330	2	C71096	probable modificat	666	6	1.8	360	2	T27694	hypothetical prote
594	6	1.8	330	2	D95958	conserved hypotet	667	6	1.8	360	2	T70863	hypothetical prote
595	6	1.8	330	4	PS0079	probable naringeni	668	6	1.8	360	2	T51870	hypothetical prote
596	6	1.8	331	2	D83480	cytochrome o ubiq	669	6	1.8	361	2	S57182	probable polygalac-
597	6	1.8	331	2	T32168	hypothetical prote	670	6	1.8	361	2	T31815	hypothetical prote
598	6	1.8	331	2	T32445	hypothetical prote	671	6	1.8	362	2	S29968	coat protein vp1 -
599	6	1.8	332	1	WMBP16	gene 16 protein -	672	6	1.8	362	2	S78515	single-stranded nu
600	6	1.8	332	1	WMBP26	gene 16 protein -	673	6	1.8	363	2	AC0244	conserved hypotet
601	6	1.8	332	2	A11691	oxidoreductases ho	674	6	1.8	364	2	F96603	hypothetical prote
602	6	1.8	332	2	A11319	oxidoreductases ho	675	6	1.8	365	2	JQ0879	NS5 protein - hepa
603	6	1.8	332	2	T23503	hypothetical prote	676	6	1.8	365	2	S42471	mRNP protein E2 -
604	6	1.8	332	2	H82064	conserved hypotet	677	6	1.8	365	2	A12940	acetyltransferase
605	6	1.8	333	2	B85667	proteinase [import	678	6	1.8	366	2	E87457	conserved hypotet
606	6	1.8	333	2	G72058	proteinase IV, pro	679	6	1.8	366	2	A55525	carboxy-cis,cis-mu
607	6	1.8	334	2	D83750	pyridoxal phosphat	680	6	1.8	366	2	T31933	hypothetical prote
608	6	1.8	334	2	S44299	hypothetical prote	681	6	1.8	367	2	B72644	probable transketo
609	6	1.8	335	2	T27658	hypothetical prote	682	6	1.8	368	2	S71190	heat shock protein
610	6	1.8	335	2	T25498	hypothetical prote	683	6	1.8	368	2	AH2694	MFS permease limpo
611	6	1.8	336	2	B49683	ptsh 3'-region pro	684	6	1.8	370	2	A60089	transforming prote
612	6	1.8	337	2	E83961	involved in fatty	685	6	1.8	370	2	S29139	aggregran - pig (fr
613	6	1.8	337	2	B88957	protein 2K697.7 [i	686	6	1.8	370	2	G90248	conserved hypotet

687 1.8 371 2 A90044
688 1.8 371 2 A53908
689 1.8 371 2 JCS498
690 1.8 371 2 G84358
691 1.8 372 1 Q0BE88
692 1.8 372 2 PQ0138
693 1.8 372 2 E84856
694 1.8 372 2 A98342
695 1.8 374 2 S40756
696 1.8 375 2 A10209
697 1.8 375 2 A12041
698 1.8 376 2 AG1410
699 1.8 376 2 G83290
700 1.8 376 2 JC6535

ALIGNMENTS

RESULT 1
H72621
hypothetical protein APE1433 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: H72621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <RNA>
A:Cross-references: DDBJ:AF000061; NID:G5104821; PIDN:BAA80430.1; PID:di044216; PID:G510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1433

Query Match 2.7%; Score 9; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 LTGSASGP 25
|||||||
DB 105 LTGSASGP 113

RESULT 2
QRMSP1
microtubule-associated protein MAP1B - mouse
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
C:Accession: S07549; S44387; A33645
R:Noble, M.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 105, 3367-3376, 1989
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B contains
A:Reference number: A33645; MUID:90094539; PMID:2480963
A:Accession: S07549
A:Molecule type: mRNA
A:Residues: 1-2464 <NOB>
A:Cross-references: EMBL:X51396; NID:G52999; PIDN:CAA35761.1; PID:G53000
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.
Arch. Biochem. Biophys. 310, 428-432, 1994
A:Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
A:Reference number: S44387; MUID:94234720; PMID:8179328
A:Accession: S44387
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 653-663, IC <SAN>
C:Superfamily: microtubule-associated protein MAP1B
C:Keywords: microtubule binding; phosphoprotein; tandem repeat

F:589-786/Domain: microtubule binding #status experimental <MTB>
F:589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-69
R-K-E/D-X)
F:1861-2064/Region: 17-residue repeats
F:91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2030,2054,2083/Binding site: ph
F:147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (co
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 2.7%; Score 9; DB 1; Length 2464;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AASGPVKEL 29
|||||||
DB 812 AASGPVKEL 820

RESULT 3
S76681
hypothetical protein - Synschochystis sp. (strain PCC 6803)
C:Species: Synschochystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76681
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synschochystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76681
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-173 <KAN>
A:Cross-references: EMBL:D64004; GB:AB001339; NID:G1001701; PIDN:BAA10625.1; PID:G120845
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: cyanelle Cyanophora paradoxa hypothetical protein ycf36

Query Match 2.4%; Score 8; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLLSLFVL 243
|||||||
DB 85 LLLSLFVL 92

RESULT 4
A82159
hypothetical protein VCI772 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: A82159
R:Heidelberger, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82159
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <HEI>
A:Cross-references: GB:AE004254; GB:AE003852; NID:G9656292; PIDN:AAF94921.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C:Genetics:
A:Gene: VCI772
A:Map position: 1

Query Match 2.4%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 EKKRVVIC 268
Db 134 EKKRVVIC 141

RESULT 5

S18733
glutenin high molecular weight chain 1bY9 precursor - wheat
C:Species: Triticum aestivum (common wheat)
C>Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C:Accession: S18733
R:Halford, N.G.; Forde, J.; Anderson, O.D.; Greene, F.C.; Shewry, P.R.
Theor. Appl. Genet. 75, 117-126, 1987
A:Title: The nucleotide and deduced amino acid sequences of an HMW glutenin subunit gene A and 1D.
A:Reference number: S18733
A:Accession: S18733
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-705 <HAL>
A:Cross-references: EMBL:X61026; NID:g22089; PIDN:CAA43361.1; PID:g22090
C:Superfamily: glutenin

Query Match 2.4%; Score 8; DB 2; Length 705;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 YSSSLQOP 115
Db 496 YSSSLQOP 503

RESULT 6

S38673
desmoglein 2 - human
N:Alternate names: desmoglein HDCC
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
C:Accession: S38673; B38872
R:Zimbelmann, R.
submitted to the EMBL Data Library, September 1993
A:Reference number: S38673
A:Accession: S38673
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1117 <ZIM>
A:Cross-references: EMBL:226317; NID:g416177; PIDN:CAA81226.1; PID:g416178
R:Koch, P.J.; Goldschmidt, M.D.; Walsh, M.J.; Zimbelmann, R.; Franke, W.W.
Eur. J. Cell Biol. 55, 200-208, 1991
A:Title: Complete amino acid sequence of the epidermal desmoglein precursor polypeptide
A:Reference number: A38872; MUID:92037656; PMID:1935985

QY 231 LLLVPLLL 238
Db 624 LLLVPLLL 631

Query Match 2.4%; Score 8; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7

T29918
hypothetical protein ZC449.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T29918
R:Latreille, P.; Gattung, S.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid ZC449.
A:Reference number: Z20708

A:Accession: T29918
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-105 <LAT>
A:Cross-references: EMBL:U41510; PIDN:AAA82633.1; CESP:ZC449.4
C:Genetics:
A:Gene: CESP:ZC449.4
A:Introns: 26/3; 51/1, 87/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC449.4

Query Match 2.1%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 MVLLCLL 232
Db 63 MVLLCLL 69

RESULT 8

E71866
hypothetical protein jhp0956 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C:Accession: E71866
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori
A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: E71866
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <ARN>
A:Cross-references: GB:AE001525; GB:AE001439; NID:g4155533; PIDN:AAD06530.1; PID:g4155533

A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0956
C:Superfamily: Helicobacter pylori hypothetical protein jhp0956

Query Match 2.1%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 PLLLSLF 241
Db 102 PLLLSLF 108

RESULT 9

AE1817
hypothetical protein all0085 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1817
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1817

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA077609.1; PID:gl7135063; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all0085

Query Match 2.1%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
|||||
Db 14 VLLCLLL 20

RESULT 10
F97283
ribosomal protein L6 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 12-Jun-2003
C;Accession: F97283
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97283
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK81057.1; PID:gl5026184; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC3118
C;Superfamily: ribosomal protein L6/L9

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KELVGSV 33
|||||
Db 139 KELVGSV 145

RESULT 11
F83305
hypothetical protein PA2724 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83305
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Buchanan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83305
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <STO>
A;Cross-references: GB:AE004700; PIDN:AAG06112.1; GSPDB:GN00179
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2724

Query Match 2.1%; Score 7; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RVDFPDG 86
|||||

Db 42 RVDFPDG 48
|||||

RESULT 12
F97499
hypothetical protein AGR_C_2123 [imported] - Agrobacterium tumefaciens (strain C58, Cerevisiae)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: F97499
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86951.1; PID:gl5156185; GSPDB:GN00169
C;Genetics:
A;Gene: AGR_C_2123
A;Map position: circular chromosome

Query Match 2.1%; Score 7; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 LLSLFVL 243
|||||
Db 34 LLSLFVL 40

RESULT 13
I40220
hypothetical protein 2 - Bacillus licheniformis (fragment)
C;Species: Bacillus licheniformis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40220
R;Harry, E.J.; Partridge, S.R.; Weiss, A.S.; Wake, R.G.
Gene 147, 85-89, 1994
A;Title: Conservation of the 168 divIB gene in Bacillus subtilis W23 and B. licheniformis
A;Reference number: I40220; MUID:94374713; PMID:8088553
A;Accession: I40220
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-184 <RES>
A;Cross-references: EMBL:U01958; NID:g404008; PIDN:AAA57244.1; PID:g404010

Query Match 2.1%; Score 7; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGGAV 37
|||||
Db 9 GSVGGAV 15

RESULT 14
H70416
hypothetical protein aq_1348 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Nov-1999
C;Accession: H70416
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V. Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70416
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <AQF>

A:Cross-references: GB:AE000736; NID:G2983763; PIDN:AAC07334.1; PID:G2983775; GB:AE00069
A:Experimental source: strain VFS

C:Genetics:
A:Gene: aq_1348

C:Superfamily: Aquifex aeolicus hypothetical protein aq_1348

Query Match 2.1%; Score 7; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLFLWFL 250
|||
Db 142 GLFLWFL 148

RESULT 15
T45543

hypothetical protein 2 [imported] - Klebsiella pneumoniae transposon Tn5711

C:Species: Klebsiella pneumoniae

C:Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 17-Mar-2000

C:Accession: T45543

R:Albiger, B.; Hubert, J.C.; Lett, M.C.
submitted to the EMBL Data Library, October 1998

A:Description: Composite transposons Tn5708 and Tn5709 are based on a Tn3-like element T

A:Reference number: Z23003

A:Accession: T45543

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-199 <ALB>

A:Cross-references: EMBL:AJ011907; PIDN:CAA09858.1

A:Experimental source: strain K111A

C:Genetics:

A:Mobile element: transposon Tn5711

C:Superfamily: bacitracin transport permease; glucose-6-phosphatase catalytic domain hom

Query Match 2.1%; Score 7; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLLSLFV 242
|||
Db 132 LLLSLFV 138

Search completed: August 18, 2004, 16:00:57

Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:53:29 ; Search time 13 seconds
(without alignments)
1341.808 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335
Sequence: 1 MAGSPCTCTLIYILQLTGS.....PHSLTMDPTPLFAYENVI 335

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.7	2464	1	MAPB_MOUSE
2	8	2.4	669	1	BGAL_FELCA
3	8	2.4	1117	1	DSG2_HUMAN
4	8	2.4	1122	1	DSG2_MOUSE
5	7	2.1	75	1	MTRF_METKA
6	7	2.1	97	1	SY08_MOUSE
7	7	2.1	98	1	SY13_HUMAN
8	7	2.1	177	1	RLIX_SPOFR
9	7	2.1	184	1	MURB_BACLI
10	7	2.1	189	1	YD48_AQUAE
11	7	2.1	228	1	UT11_ARATH
12	7	2.1	239	1	YTM1_BACSU
13	7	2.1	266	1	FLIP_CAUCR
14	7	2.1	293	1	CFXO_GUITH
15	7	2.1	300	1	MURB_STR3
16	7	2.1	301	1	MURB_BACHD
17	7	2.1	303	1	MURB_BACSU
18	7	2.1	305	1	MURB_CLOAB
19	7	2.1	312	1	APE_RAT
20	7	2.1	316	1	MURB_STRPN
21	7	2.1	356	1	COX2_BACSU
22	7	2.1	362	1	ASG2_YEAST
23	7	2.1	367	1	GLNA_CAEEL
24	7	2.1	381	1	CYB_ISUPA
25	7	2.1	381	1	CYB_SCYCA
26	7	2.1	381	1	CYB_RHIME
27	7	2.1	418	1	MTR_HAEIN
28	7	2.1	433	1	YBL4_YEAST
29	7	2.1	448	1	GNTF_BACLI
30	7	2.1	507	1	D7A1_MALDO
31	7	2.1	508	1	PD12_ARATH
32	7	2.1	515	1	SIR2_CANAL
33	7	2.1	539	1	RIK2_MOUSE

34	7	2.1	540	1	RIK2_HUMAN
35	7	2.1	586	1	ENV_MPMV
36	7	2.1	587	1	ENV_SRV1
37	7	2.1	591	1	CALX_MOUSE
38	7	2.1	591	1	CALX_RAT
39	7	2.1	604	1	PGH2_CAVPO
40	7	2.1	605	1	PCOA_ECOLI
41	7	2.1	650	1	LIB1_HUMAN
42	7	2.1	675	1	HPPA_XANAC
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44	7	2.1	732	1	ACPH_HUMAN
45	7	2.1	739	1	FTSK_TREPA
46	7	2.1	914	1	PBPA_BACSU
47	7	2.1	943	1	UVRA_STRPN
48	7	2.1	954	1	GCSP_AGR75
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50	7	2.1	954	1	GCSP_SYNEL
51	7	2.1	954	1	GCSP_VIBPA
52	7	2.1	954	1	GCSP_VIBVU
53	7	2.1	956	1	GCSP_ECO57
54	7	2.1	956	1	GCSP_ECOLI
55	7	2.1	956	1	GCSP_ECOLI
56	7	2.1	956	1	GCSP_SALTI
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69	7	2.1	1025	1	GCSP_MOUSE
70	7	2.1	1032	1	MT18_YEAST
71	7	2.1	1085	1	IFH1_YEAST
72	7	2.1	1210	1	PER3_HUMAN
73	7	2.1	1269	1	FLIH_HUMAN
74	7	2.1	1290	1	PER1_HUMAN
75	7	2.1	1291	1	PER1_MOUSE
76	7	2.1	1312	1	DPOL_PYRSD
77	7	2.1	1581	1	PRRB_HUMAN
78	7	2.1	2787	1	TEL1_YEAST
79	6	1.8	49	1	LHA7_RHOAC
80	6	1.8	52	1	CD3E_BOVIN
81	6	1.8	61	1	NOL4_PEA
82	6	1.8	70	1	BGB1_DROME
83	6	1.8	83	1	PRRP_RAT
84	6	1.8	84	1	RL27_CHLTE
85	6	1.8	92	1	YA50_HAEIN
86	6	1.8	95	1	CH10_ALTHA
87	6	1.8	96	1	CH10_ACTAC
88	6	1.8	96	1	CH10_ACTPL
89	6	1.8	96	1	CH10_BUCAL
90	6	1.8	96	1	CH10_BUCAP
91	6	1.8	96	1	CH10_BUCWP
92	6	1.8	96	1	CH10_HAEIN
93	6	1.8	96	1	CH10_PASMU
94	6	1.8	96	1	CH10_SHEON
95	6	1.8	96	1	CH11_VIBCH
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97	6	1.8	96	1	CH11_VIBVU
98	6	1.8	96	1	VGE_BPG4
99	6	1.8	97	1	CH10_BUCBP
100	6	1.8	97	1	CH10_BUCGU
101	6	1.8	97	1	CH10_BUCPP
102	6	1.8	97	1	CH10_BUCPS
103	6	1.8	97	1	CH10_BUCTC
104	6	1.8	97	1	CH10_BUCTS
105	6	1.8	97	1	CH10_BUCTI
106	6	1.8	97	1	CH10_ECOLI

043353	h	receptor-
P07575	simian	maso
P04027	simian	retr
P35564	mus	musculus
P35565	rattus	norv
P70882	cavia	porce
Q84452	escherichia	
Q84452	h	leukocyte
Q84452	xanthomonas	
Q84452	xanthomonas	
P13798	homo	sapien
Q83964	trichomonas	p
P39793	trichomonas	p
Q84452	streptococcus	
Q84452	agrobacterium	
Q84452	rhizobium	m
Q84452	synecococcus	
Q84452	vibrio	para
Q84452	vibrio	vuln
Q84452	escherichia	
Q84452	escherichia	
P33195	escherichia	
Q84452	salmonella	
Q84452	salmonella	
Q84452	pseudomonas	
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Q84452	versinia	pe
Q84452	thermus	the
Q84452	xanthomonas	
Q84452	xanthomonas	
P56722	bos	taurus
Q84452	raletonia	s
P48526	saccharomyc	
Q75665	homo	sapien
P23378	homo	sapien
Q91443	mus	musculus
P40469	saccharomyc	
P39520	saccharomyc	
P56645	homo	sapien
Q13045	homo	sapien
Q15534	homo	sapien
Q35973	mus	musculus
Q51334	pyrococcus	
Q15648	h	peroxisom
P38110	saccharomyc	
P35093	rhodospseudo	
Q28073	bos	taurus
P26415	pisum	sativ
P38040	drosophila	
P81278	rattus	norv
Q84452	chlorobium	
P71365	haemophilus	
Q9422	actinobacil	
P46399	actinobacil	
P94165	actinobacil	
P25749	buchnera	ap
Q59176	buchnera	ap
Q51831	buchnera	ap
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Q59686	pasteurella	
Q84452	shewanella	
Q94412	vibrio	chol
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107	1.8	97	1	CH10_ENTAE	Q93fu7 enterobacte	180	1.8	166	1	NU6M DINSE	O79557 dinodon sem
108	1.8	97	1	CH10_SALTY	Q9lc51 salmonella	181	1.8	171	1	PABA_BHILO	Q98bh8 rhizobium l
109	1.8	97	1	CH10_WIGER	Q9ans0 wiggleswort	182	1.8	171	1	Y079_DEIRA	Q9ry71 deinococcus
110	1.8	97	1	CH10_XANWA	P95801 xanthomonas	183	1.8	172	1	NU6M_RAT	P03326 rattus norv
111	1.8	97	1	GAC2_CLOAB	Q97ex7 clostridium	184	1.8	172	1	Y442_CHLPN	Q928a1 chlamydia p
112	1.8	97	1	SY07_MOUSE	Q03366 mus musculus	185	1.8	176	1	PNOC_BOVIN	O62647 bos taurus
113	1.8	98	1	NULM_BALMU	P41301 balaenopter	186	1.8	176	1	PNOC_HUMAN	Q13519 homo sapien
114	1.8	98	1	NULM_BALPH	P24976 balaenopter	187	1.8	176	1	PRND_HUMAN	Q9uky0 homo sapien
115	1.8	98	1	NULM_RABIT	O79435 cryptotagus	188	1.8	177	1	RLIX_DROME	P41093 drosophila
116	1.8	98	1	MRP1_BOVIN	P81264 bos taurus	189	1.8	184	1	IPYR_MYCPN	P75250 mycoplasma
117	1.8	99	1	MCPA_BOVIN	P28291 bos sapien	190	1.8	184	1	DEF2_NITEU	Q82tc8 nitrosomona
118	1.8	99	1	SY02_HUMAN	P13500 homo sapien	191	1.8	185	1	FAPR_STAEP	O8csv2 staphylococ
119	1.8	99	1	SY02_WACFA	Q9myr4 macaca fasc	192	1.8	186	1	HS23_DROME	P02516 drosophila
120	1.8	99	1	SY02_PIG	P28331 sus scrofa	193	1.8	186	1	FAPR_STAEP	O8csv2 staphylococ
121	1.8	99	1	SY07_HUMAN	P80098 homo sapien	194	1.8	186	1	HS23_DROME	P02516 drosophila
122	1.8	99	1	SY08_BOVIN	Q09141 bos sapien	195	1.8	186	1	FAPR_STAEP	O8csv2 staphylococ
123	1.8	99	1	SY08_HUMAN	P80075 homo sapien	196	1.8	186	1	FAPR_STAEP	O8csv2 staphylococ
124	1.8	99	1	SY08_PIG	P49873 sus scrofa	197	1.8	186	1	FAPR_STAEP	O8csv2 staphylococ
125	1.8	100	1	NUOK_ECOLI	P33606 escherichia	198	1.8	188	1	RERI_YEAST	P25560 saccharomyc
126	1.8	100	1	YJCE_BACSU	O31627 bacillus su	199	1.8	188	1	RERI_YEAST	P25560 saccharomyc
127	1.8	101	1	SY02_CANFA	P52203 canis fami	200	1.8	188	1	RERI_YEAST	P25560 saccharomyc
128	1.8	101	1	YGVA_YEAST	P53089 saccharomyc	201	1.8	188	1	RERI_YEAST	P25560 saccharomyc
129	1.8	102	1	CH11_VIBHA	Q83wi9 vibrio harv	202	1.8	188	1	RERI_YEAST	P25560 saccharomyc
130	1.8	104	1	SY12_MOUSE	O62401 mus muscul	203	1.8	188	1	RERI_YEAST	P25560 saccharomyc
131	1.8	108	1	YCS4_PORPU	P51204 porphyra pu	204	1.8	188	1	RERI_YEAST	P25560 saccharomyc
132	1.8	111	1	RBFA_HELPJU	Q92m45 helicobacte	205	1.8	188	1	RERI_YEAST	P25560 saccharomyc
133	1.8	111	1	RBFA_HELPFY	O25688 helicobacte	206	1.8	188	1	RERI_YEAST	P25560 saccharomyc
134	1.8	113	1	MIH_CALSI	P55321 callinectes	207	1.8	188	1	RERI_YEAST	P25560 saccharomyc
135	1.8	115	1	IR03_HCMVA	P16802 human cytom	208	1.8	188	1	RERI_YEAST	P25560 saccharomyc
136	1.8	118	1	VAG1_PANTR	Q862z6 pan troglod	209	1.8	188	1	RERI_YEAST	P25560 saccharomyc
137	1.8	118	1	VAG2_HUMAN	O95670 homo sapien	210	1.8	188	1	RERI_YEAST	P25560 saccharomyc
138	1.8	118	1	VAG2_MOUSE	Q9wtt4 mus muscul	211	1.8	188	1	RERI_YEAST	P25560 saccharomyc
139	1.8	118	1	VAG2_PIG	Q9tev6 sus scrofa	212	1.8	188	1	RERI_YEAST	P25560 saccharomyc
140	1.8	120	1	SY02_CAVPO	Q08782 cavia porce	213	1.8	188	1	RERI_YEAST	P25560 saccharomyc
141	1.8	120	1	YMG6_RHIME	Q92u95 rhizobium m	214	1.8	188	1	RERI_YEAST	P25560 saccharomyc
142	1.8	123	1	YI19_RHIME	Q92vb9 rhizobium m	215	1.8	188	1	RERI_YEAST	P25560 saccharomyc
143	1.8	124	1	APC4_RABIT	P55057 cryptotagus	216	1.8	188	1	RERI_YEAST	P25560 saccharomyc
144	1.8	124	1	KABI_OLDAF	P56254 oldenlandia	217	1.8	188	1	RERI_YEAST	P25560 saccharomyc
145	1.8	125	1	SY02_RABIT	P28292 cryptotagus	218	1.8	188	1	RERI_YEAST	P25560 saccharomyc
146	1.8	126	1	NUOA_BUCAP	Q8ky97 buchnera ap	219	1.8	188	1	RERI_YEAST	P25560 saccharomyc
147	1.8	126	1	YIGF_ECOLI	P27842 escherichia	220	1.8	188	1	RERI_YEAST	P25560 saccharomyc
148	1.8	126	1	YIGF_SALTY	P31139 salmonella	221	1.8	188	1	RERI_YEAST	P25560 saccharomyc
149	1.8	128	1	MERT_STAUA	P08656 staphylococ	222	1.8	188	1	RERI_YEAST	P25560 saccharomyc
150	1.8	128	1	Y384_HSVMG	Q9cns3 pasteurella	223	1.8	188	1	RERI_YEAST	P25560 saccharomyc
151	1.8	128	1	Y393_PASMO	Q9rn06 bacillus an	224	1.8	188	1	RERI_YEAST	P25560 saccharomyc
152	1.8	130	1	YQ26_BACAN	Q8z7q6 salmonella	225	1.8	188	1	RERI_YEAST	P25560 saccharomyc
153	1.8	136	1	YEDX_SALTY	Q8x575 escherichia	226	1.8	188	1	RERI_YEAST	P25560 saccharomyc
154	1.8	136	1	YEDX_SALTY	P76341 escherichia	227	1.8	188	1	RERI_YEAST	P25560 saccharomyc
155	1.8	137	1	YEDX_ECO57	P76341 escherichia	228	1.8	188	1	RERI_YEAST	P25560 saccharomyc
156	1.8	137	1	YEDX_ECOLI	P24511 drosophila	229	1.8	188	1	RERI_YEAST	P25560 saccharomyc
157	1.8	141	1	CH16_DROSU	P00716 cryptotagus	230	1.8	188	1	RERI_YEAST	P25560 saccharomyc
158	1.8	141	1	LCA_RABIT	O02376 haemochus	231	1.8	188	1	RERI_YEAST	P25560 saccharomyc
159	1.8	141	1	RL9_HABCO	O88969 rattus norv	232	1.8	188	1	RERI_YEAST	P25560 saccharomyc
160	1.8	142	1	CST8_RAT	Q88969 rattus norv	233	1.8	188	1	RERI_YEAST	P25560 saccharomyc
161	1.8	142	1	RUVA_MYCPE	Q88969 rattus norv	234	1.8	188	1	RERI_YEAST	P25560 saccharomyc
162	1.8	143	1	IL4_MERUN	P47966 meriones un	235	1.8	188	1	RERI_YEAST	P25560 saccharomyc
163	1.8	145	1	SJ2E_HUMAN	P57105 homo sapien	236	1.8	188	1	RERI_YEAST	P25560 saccharomyc
164	1.8	146	1	HBB1_UROHA	P18991 uromastix h	237	1.8	188	1	RERI_YEAST	P25560 saccharomyc
165	1.8	146	1	RL15_MYCLE	O33002 mycobacteri	238	1.8	188	1	RERI_YEAST	P25560 saccharomyc
166	1.8	146	1	YS55_CABEL	Q09664 caenorhabd	239	1.8	188	1	RERI_YEAST	P25560 saccharomyc
167	1.8	151	1	YHR6_YEAST	P38824 saccharomyc	240	1.8	188	1	RERI_YEAST	P25560 saccharomyc
168	1.8	153	1	GIP_HUMAN	P09681 homo sapien	241	1.8	188	1	RERI_YEAST	P25560 saccharomyc
169	1.8	153	1	Y587_METJA	Q58007 methanococ	242	1.8	188	1	RERI_YEAST	P25560 saccharomyc
170	1.8	158	1	IPYR_COREF	Q8fmf8 corynebacte	243	1.8	188	1	RERI_YEAST	P25560 saccharomyc
171	1.8	158	1	IPYR_COREG	Q8nm79 corynebacte	244	1.8	188	1	RERI_YEAST	P25560 saccharomyc
172	1.8	160	1	RSBW_BACLI	O50231 bacillus li	245	1.8	188	1	RERI_YEAST	P25560 saccharomyc
173	1.8	161	1	SH1B_CANFA	P79250 canis fami	246	1.8	188	1	RERI_YEAST	P25560 saccharomyc
174	1.8	162	1	PHCA_AGLNE	P28557 aglaothammi	247	1.8	188	1	RERI_YEAST	P25560 saccharomyc
175	1.8	162	1	PHCA_GALSU	P00306 galdieria s	248	1.8	188	1	RERI_YEAST	P25560 saccharomyc
176	1.8	162	1	PHCA_MASIA	P00307 mastigoclad	249	1.8	188	1	RERI_YEAST	P25560 saccharomyc
177	1.8	163	1	PHCA_ANASP	P07121 anabaena sp	250	1.8	188	1	RERI_YEAST	P25560 saccharomyc
178	1.8	164	1	CGHB_CALJA	P51500 callithrix	251	1.8	188	1	RERI_YEAST	P25560 saccharomyc
179	1.8	165	1	MSRA_UREPA	Q9pqk2 ureaplasma	252	1.8	188	1	RERI_YEAST	P25560 saccharomyc

253	6	1.8	269	1	RIBF_MYCPN	P75587 mycoplasma	326	6	1.8	337	1	PLSX_BACHD	Q9ka01 bacillus ha
254	6	1.8	270	1	FWDC_METTM	Q59579 methanobact	327	6	1.8	339	1	MDH_METFE	P16142 methanother
255	6	1.8	273	1	FWDC_METJA	Q58571 methanococc	328	6	1.8	339	1	RIR2_MYCPN	P75461 mycoplasma
256	6	1.8	275	1	IC2A_HUMAN	P13598 homo sapien	329	6	1.8	340	1	RIR2_MYCGE	P47471 mycoplasma
257	6	1.8	276	1	ATP6_SVNY3	P21798 synecocyst	330	6	1.8	342	1	HUPV_AZOGH	Q43959 azotobacter
258	6	1.8	276	1	DHCA_MOUSE	P48758 mus musculus	331	6	1.8	342	1	TORT_ECO57	P58358 escherichia
259	6	1.8	276	1	NUGN_CANMA	Q00673 candida mal	332	6	1.8	342	1	TORT_ECOLI	P38683 escherichia
260	6	1.8	278	1	OX2G_HUMAN	P41217 homo sapien	333	6	1.8	344	1	TORT_ECOLI	Q9hh89 halobacteri
261	6	1.8	278	1	OX2G_MOUSE	O54901 mus musculus	334	6	1.8	345	1	GVN2_HALN2	P33965 halobacteri
262	6	1.8	278	1	OX2G_RAT	O42018 rattus norv	335	6	1.8	347	1	FOS_CYPCA	P79702 cyprinus ca
263	6	1.8	280	1	KDSA_NEIMA	Q9lju48 n 2-dehydro	336	6	1.8	347	1	NUZM_DUGDU	O8w9p5 dugong dugo
264	6	1.8	280	1	KDSA_NEIMB	Q9cjd55 n 2-dehydro	337	6	1.8	347	1	NUZM_RABIT	O79428 oryctolagus
265	6	1.8	281	1	YQAC_LACLA	Q9cfb9 lactococcus	338	6	1.8	350	1	DKK3_HUMAN	O79428 oryctolagus
266	6	1.8	282	1	VMSA_HVHW6	P11293 woodchuck h	339	6	1.8	350	1	GLCE_ECOLI	P52073 escherichia
267	6	1.8	284	1	MURB_THEMEA	Q9x239 thermotoga	340	6	1.8	350	1	HN3G_HUMAN	P55318 homo sapien
268	6	1.8	284	1	YNFH_ECOLI	P76173 escherichia	341	6	1.8	351	1	HSF3_LYCPE	P41152 helicobact
269	6	1.8	286	1	MEPA_HAEIN	P44566 haemophilus	342	6	1.8	351	1	SPIN_HAEPV	O05894 heliothis a
270	6	1.8	286	1	PTND_ECOLI	P08188 escherichia	343	6	1.8	352	1	DHSO_BACSU	Q06004 bacillus su
271	6	1.8	287	1	XT14_ARATH	Q9z8u4 arabidopsis	344	6	1.8	352	1	WNT2_DROME	P28465 drosophila
272	6	1.8	288	1	PCD1_MOUSE	Q02242 mus musculus	345	6	1.8	353	1	CKR8_MOUSE	P56484 mus musculus
273	6	1.8	288	1	PTR1_LEIMA	Q01782 leishmania	346	6	1.8	354	1	MURB_TREPA	O83128 treponema p
274	6	1.8	288	1	SP4G_BACSU	P26937 bacillus su	347	6	1.8	354	1	PHOB_ECOLI	P31544 escherichia
275	6	1.8	289	1	PTR1_LEITA	P42556 leishmania	348	6	1.8	355	1	AMBP_PLEPL	P36992 pleuronecte
276	6	1.8	290	1	NANA_FUSNN	Q8rdn6 fusobacteri	349	6	1.8	356	1	PCB1_HUMAN	Q15365 homo sapien
277	6	1.8	290	1	PRNA_FORGI	P60093 porphyromon	350	6	1.8	356	1	PCB1_RABIT	O19048 oryctolagus
278	6	1.8	292	1	V226_FOWPV	Q94509 fowlpox vir	351	6	1.8	357	1	ID12_CHLTE	O8kf55 chlorobium
279	6	1.8	293	1	BLAC_RHOCA	P14171 rhodobacter	352	6	1.8	358	1	ILVE_STAMP	O99w55 staphylococ
280	6	1.8	293	1	RK4_SPIOL	O49937 spinacia ol	353	6	1.8	358	1	ILVE_STAEP	O99w55 staphylococ
281	6	1.8	296	1	MURB_CHLVC	O822b0 chlamydophi	354	6	1.8	358	1	RF1_STRCO	O8c978 staphylococ
282	6	1.8	296	1	RFBP_SHIFL	P37782 shigella fi	355	6	1.8	360	1	YS03_CABEL	Q9k464 streptomyce
283	6	1.8	297	1	BXD1_CABEL	Q9n3f0 caenorhabdi	356	6	1.8	361	1	PGLR_YEAST	Q93358 caenorhabdi
284	6	1.8	297	1	IC1A_ECOLI	P24194 escherichia	357	6	1.8	361	1	RM45_DROME	P47180 saccharomyc
285	6	1.8	297	1	IC1A_EDWIC	O52399 edwardsiell	358	6	1.8	362	1	PCB2_MOUSE	O9vcx3 saccharophi
286	6	1.8	297	1	IC1A_SALTI	P58508 salmonella	359	6	1.8	363	1	AROB_STRAW	O61990 mus musculu
287	6	1.8	297	1	IC1A_SALTY	P58509 salmonella	360	6	1.8	363	1	AROB_STRCO	O827r8 streptomyce
288	6	1.8	297	1	MURB_AQUAE	Q66805 aquifex aeo	361	6	1.8	365	1	CMLE_NEUCR	Q9kxq6 streptomyce
289	6	1.8	298	1	MIME_HUMAN	P20774 homo sapien	362	6	1.8	365	1	PCB2_HUMAN	P38677 neurospora
290	6	1.8	298	1	YSNK_CABEL	Q19408 caenorhabdi	363	6	1.8	371	1	CM1_MOUSE	Q15366 homo sapien
291	6	1.8	299	1	T2R1_CERAE	Q8mjue cercopithe	364	6	1.8	371	1	TRM1_HALN1	P97468 mus musculu
292	6	1.8	302	1	IC1A_YERPE	P58510 yersinia pe	365	6	1.8	372	1	HS72_PARLI	P97705 halobacteri
293	6	1.8	302	1	MURB_LACPL	O88yf4 lactobacill	366	6	1.8	372	1	MURG_CORGL	P22623 paracentrot
294	6	1.8	303	1	HYPB_AZOVI	P31880 azotobacter	367	6	1.8	372	1	VGLI_HSV23	Q8nnn5 corynebacte
295	6	1.8	304	1	MURB_CHLPN	Q92681 chlamydia p	368	6	1.8	372	1	VGLI_HSV23	P06784 herpes simp
296	6	1.8	305	1	HYPB_AZOGH	Q43949 azotobacter	369	6	1.8	374	1	NIR_RHOSH	Q96cd0 homo sapien
297	6	1.8	307	1	MURB_OCEIH	Q8eer4 oceanobacil	370	6	1.8	376	1	PSD4_MOUSE	O53239 rhodobacter
298	6	1.8	308	1	CAH6_HUMAN	P23280 homo sapien	371	6	1.8	377	1	PSD4_HUMAN	O35236 mus musculu
299	6	1.8	311	1	HEN3_VIBCH	Q9kvm1 vibrio chol	372	6	1.8	377	1	Y392_CHLTR	P55036 homo sapien
300	6	1.8	311	1	MENA_BACSU	P39582 bacillus su	373	6	1.8	379	1	CYB_GALMO	P36427 chlamydia t
301	6	1.8	311	1	PTX1_CHICK	P56673 gallus gall	374	6	1.8	380	1	DSVB_DESVH	Q999j6 galago moho
302	6	1.8	311	1	SPAC_STRPN	Q97pr8 streptococc	375	6	1.8	386	1	SH1B_MOUSE	P44575 desulfovibr
303	6	1.8	313	1	SPV1_MOUSE	Q9gxv9 mus musculu	376	6	1.8	386	1	SH1B_RAT	P28334 mus musculu
304	6	1.8	314	1	RLA0_THEAC	P57692 thermoplas	377	6	1.8	386	1	SH1B_SPAEH	P28564 rattus norv
305	6	1.8	315	1	O8J3_HUMAN	Q8ng90 homo sapien	378	6	1.8	387	1	SGCA_HUMAN	P56496 spalax leuc
306	6	1.8	316	1	O8J1_HUMAN	Q8ngp2 homo sapien	379	6	1.8	387	1	SGCA_MESAU	Q16586 homo sapien
307	6	1.8	318	1	KDGT_XANAC	P89q16 xanthomonas	380	6	1.8	387	1	SGCA_MOUSE	Q64255 mesocricetu
308	6	1.8	319	1	NULM_VARFL	Q94vi4 varanus fla	381	6	1.8	387	1	SGCA_RABIT	P82350 mus musculu
309	6	1.8	324	1	KDGG_BACSU	P50845 bacillus su	382	6	1.8	388	1	SH1B_DDMA	O28686 oryctolagus
310	6	1.8	324	1	NAS4_ARATH	Q9c7x5 arabidopsis	383	6	1.8	390	1	SH1B_HUMAN	P35404 didelphia m
311	6	1.8	325	1	SYGA_RALSO	Q8y211 raistonia s	384	6	1.8	390	1	SH1B_PANTR	P28222 homo sapien
312	6	1.8	326	1	VPR1_USRV	P31625 sheep pulmo	385	6	1.8	390	1	SH1B_RABIT	P60020 pan troglod
313	6	1.8	327	1	CI30_HUMAN	Q9y375 homo sapien	386	6	1.8	390	1	VGLI_HSV11	P49144 oryctolagus
314	6	1.8	327	1	YQ80_BACAN	Q9rmv5 bacillus an	387	6	1.8	391	1	POLG_CYVV	P06487 herpes simp
315	6	1.8	328	1	YJ77_YEAST	P71145 saccharomyc	388	6	1.8	393	1	STAD_ELAGV	P20177 clover yell
316	6	1.8	331	1	PLSX_CHLTE	Q8kap3 chlorobium	389	6	1.8	394	1	PGCA_RABIT	O24428 elaeis guin
317	6	1.8	332	1	VG16_BPPHA	P11014 bacterioph	390	6	1.8	396	1	HEW3_HALN1	Q28670 oryctolagus
318	6	1.8	332	1	VG16_BPPZA	P07541 bacterioph	391	6	1.8	396	1	Y111_METJA	Q9hm55 halobacteri
319	6	1.8	334	1	PDXA_BACHD	Q9rc88 bacillus ha	392	6	1.8	397	1	ARGD_NEIMB	O57575 methanococc
320	6	1.8	335	1	LEP4_MYCHA	O30387 myxococcus	393	6	1.8	398	1	ARGD_NEIMA	Q9jtx9 neisseria m
321	6	1.8	335	1	Y7C9_BORBR	O06702 bordetella	394	6	1.8	398	1	FRHA_METVO	Q9jyv4 neisseria m
322	6	1.8	336	1	YPH1_MYCCA	P45613 mycoplasma	395	6	1.8	398	1	SHBG_RABIT	Q00350 methanococc
323	6	1.8	337	1	GP26_HUMAN	Q8rdv2 homo sapien	396	6	1.8	399	1	METK_BACHD	P15196 oryctolagus
324	6	1.8	337	1	GP26_MOUSE	Q8bza7 mus musculu	397	6	1.8	400	1	ISDF_AGRT5	Q9k7q9 bacillus ha
325	6	1.8	337	1	GP26_RAT	Q9gxix3 rattus norv	398	6	1.8	400	1	TYRP_HABIN	O8uff4 a iepd/iepf
													P44727 haemophilus

399	1.8	402	1	YJ93_PSEAE	Q912b6 pseudomonas	472	1	KCCG_HUMAN	Q13555 homo sapien
400	1.8	404	1	ALR_RICPR	Q9ae52 rickettsia	473	1	KCCG_HUMAN	P56273 xenopus lae
401	1.8	404	1	METK_PIRAB	Q9vlp7 pyrococcus	473	1	KCCG_HUMAN	P06414 marchantia
402	1.8	404	1	METK_PIRAB	Q9vlp7 pyrococcus	474	1	KCCG_HUMAN	P55356 rhizobium s
403	1.8	406	1	RL48_ARATH	Q96f40 arabidopsis	475	1	KCCG_HUMAN	P55108 rattus norv
404	1.8	406	1	RL48_ARATH	Q96f40 arabidopsis	476	1	KCCG_HUMAN	Q52892 rhizobium m
405	1.8	409	1	MDP1_PIG	P22412 sus scrofa	476	1	KCCG_HUMAN	Q32323 rhodospheudo
406	1.8	409	1	MDP1_PIG	P22412 sus scrofa	477	1	KCCG_HUMAN	Q13862 schizosacch
407	1.8	409	1	Y774_METJA	O58184 methanococc	478	1	KCCG_HUMAN	O13862 schizosacch
408	1.8	412	1	AAZA_CANFA	P11617 canis famil	478	1	KCCG_HUMAN	P24532 streptomyce
409	1.8	412	1	AAZA_HUMAN	P29274 homo sapien	480	1	KCCG_HUMAN	Q96ey1 homo sapien
410	1.8	413	1	ARGJ_STAAM	Q99x38 s arginine	480	1	KCCG_HUMAN	Q99m87 mus musculu
411	1.8	413	1	ARGJ_STAAM	Q99x38 s arginine	481	1	KCCG_HUMAN	Q6734 streptomyce
412	1.8	414	1	GAG2_DROME	O8nym7 s arginine	481	1	KCCG_HUMAN	Q9kvd9 vibrio chol
413	1.8	415	1	ILSR_MOUSE	P21883 mus musculu	482	1	KCCG_HUMAN	Q9kvd9 vibrio chol
414	1.8	415	1	ILSR_MOUSE	P21883 mus musculu	482	1	KCCG_HUMAN	Q9kvd9 vibrio chol
415	1.8	415	1	SCB2_CABEL	P53589 caenorhabdi	484	1	KCCG_HUMAN	Q18493 caenorhabdi
416	1.8	416	1	AROA_BETVU	O28775 archaeoglob	484	1	KCCG_HUMAN	P33008 pseudomonas
417	1.8	416	1	AROA_BETVU	O28775 archaeoglob	484	1	KCCG_HUMAN	Q9y916 aeropyrum p
418	1.8	417	1	IE63_HSVSA	O81919 beta vulgar	488	1	KCCG_HUMAN	P71364 haemophilus
419	1.8	417	1	PGCB_FELCA	P13199 herpesvirus	488	1	KCCG_HUMAN	Q9vzu2 deinococcus
420	1.8	419	1	KDAP_MOUSE	P41725 felis silve	490	1	KCCG_HUMAN	Q9vzu2 deinococcus
421	1.8	420	1	FLA8_ARATH	O09043 mus musculu	490	1	KCCG_HUMAN	Q9vzu2 deinococcus
422	1.8	421	1	FLA8_ARATH	O09043 mus musculu	490	1	KCCG_HUMAN	Q9vzu2 deinococcus
423	1.8	422	1	V1BR_MOUSE	Q34456 bacillus su	491	1	KCCG_HUMAN	Q9vzu2 deinococcus
424	1.8	422	1	EXUT_BACSU	O34456 bacillus su	491	1	KCCG_HUMAN	Q9vzu2 deinococcus
425	1.8	424	1	NODC_RHILLO	P23491 mesocricetu	491	1	KCCG_HUMAN	Q9vzu2 deinococcus
426	1.8	426	1	VMSA_WHV1	P17862 rhizobium l	493	1	KCCG_HUMAN	Q9vzu2 deinococcus
427	1.8	428	1	VMSA_HPBGS	P03143 woodchuck h	493	1	KCCG_HUMAN	Q9vzu2 deinococcus
428	1.8	429	1	PEPB_VIBCH	P03144 ground squi	493	1	KCCG_HUMAN	Q9vzu2 deinococcus
429	1.8	431	1	VMSA_WHV59	Q9ktx5 vibrio chol	500	1	KCCG_HUMAN	Q9vzu2 deinococcus
430	1.8	431	1	VMSA_WHV7	P12910 woodchuck h	501	1	KCCG_HUMAN	Q9vzu2 deinococcus
431	1.8	431	1	VMSA_WHV8	P12909 woodchuck h	502	1	KCCG_HUMAN	Q9vzu2 deinococcus
432	1.8	431	1	VMSA_WHV8	P08432 woodchuck h	503	1	KCCG_HUMAN	Q9vzu2 deinococcus
433	1.8	432	1	PEPB_VIBPA	P17400 woodchuck h	504	1	KCCG_HUMAN	Q9vzu2 deinococcus
434	1.8	432	1	PEPB_VIBPA	P17400 woodchuck h	505	1	KCCG_HUMAN	Q9vzu2 deinococcus
435	1.8	436	1	PEPB_VIBPA	Q987s21 vibrio para	506	1	KCCG_HUMAN	Q9vzu2 deinococcus
436	1.8	436	1	PEPB_VIBPA	Q987s21 vibrio para	507	1	KCCG_HUMAN	Q9vzu2 deinococcus
437	1.8	437	1	EFIA_AERPE	P58475 yersinia pe	507	1	KCCG_HUMAN	Q9vzu2 deinococcus
438	1.8	437	1	EFIA_AERPE	P58475 yersinia pe	508	1	KCCG_HUMAN	Q9vzu2 deinococcus
439	1.8	442	1	LEU2_BUCUS	Q9vav0 aeropyrum p	509	1	KCCG_HUMAN	Q9vzu2 deinococcus
440	1.8	442	1	LEU2_BUCUS	Q9vav0 aeropyrum p	509	1	KCCG_HUMAN	Q9vzu2 deinococcus
441	1.8	444	1	ASSY_HAEIN	P44315 haemophilus	510	1	KCCG_HUMAN	Q9vzu2 deinococcus
442	1.8	445	1	ASSY_BRAJA	P59607 bradyrhizob	511	1	KCCG_HUMAN	Q9vzu2 deinococcus
443	1.8	445	1	ASSY_PASMU	P57877 pasteurella	511	1	KCCG_HUMAN	Q9vzu2 deinococcus
444	1.8	445	1	ASSY_PASMU	P57877 pasteurella	511	1	KCCG_HUMAN	Q9vzu2 deinococcus
445	1.8	446	1	ASSY_ECO57	Q8xwcl1 raistonia s	517	1	KCCG_HUMAN	Q9vzu2 deinococcus
446	1.8	446	1	ASSY_ECOLI	Q8x9m0 escherichia	517	1	KCCG_HUMAN	Q9vzu2 deinococcus
447	1.8	446	1	ASSY_ECOLI	Q8x9m0 escherichia	517	1	KCCG_HUMAN	Q9vzu2 deinococcus
448	1.8	446	1	ASSY_SALTY	Q8x3h5 salmonella	519	1	KCCG_HUMAN	Q9vzu2 deinococcus
449	1.8	446	1	ASSY_SALTY	Q8x3h5 salmonella	520	1	KCCG_HUMAN	Q9vzu2 deinococcus
450	1.8	446	1	ASSY_SALTY	Q8x3h5 salmonella	520	1	KCCG_HUMAN	Q9vzu2 deinococcus
451	1.8	447	1	ASSY_NEIMA	P59609 shigella fl	522	1	KCCG_HUMAN	Q9vzu2 deinococcus
452	1.8	447	1	ASSY_NEIMA	P59609 shigella fl	522	1	KCCG_HUMAN	Q9vzu2 deinococcus
453	1.8	449	1	GSBN_DROME	Q9jwml1 neisseria m	524	1	KCCG_HUMAN	Q9vzu2 deinococcus
454	1.8	449	1	GSBN_DROME	Q9jwml1 neisseria m	524	1	KCCG_HUMAN	Q9vzu2 deinococcus
455	1.8	449	1	QSEC_ECOLI	P32083 drosophila	526	1	KCCG_HUMAN	Q9vzu2 deinococcus
456	1.8	449	1	QSEC_ECOLI	P32083 drosophila	526	1	KCCG_HUMAN	Q9vzu2 deinococcus
457	1.8	449	1	QSEC_ECOLI	P32083 drosophila	526	1	KCCG_HUMAN	Q9vzu2 deinococcus
458	1.8	451	1	Y037_MYCPN	Q8x524 escherichia	527	1	KCCG_HUMAN	Q9vzu2 deinococcus
459	1.8	451	1	Y037_MYCPN	Q8x524 escherichia	527	1	KCCG_HUMAN	Q9vzu2 deinococcus
460	1.8	454	1	ASSY_AERPE	P40719 escherichia	528	1	KCCG_HUMAN	Q9vzu2 deinococcus
461	1.8	454	1	ASSY_AERPE	P40719 escherichia	528	1	KCCG_HUMAN	Q9vzu2 deinococcus
462	1.8	459	1	ZPR1_SCHPO	Q8x3p2 salmonella	530	1	KCCG_HUMAN	Q9vzu2 deinococcus
463	1.8	460	1	ILGA_MOUSE	Q8x3p2 salmonella	530	1	KCCG_HUMAN	Q9vzu2 deinococcus
464	1.8	461	1	Y608_HAEIN	P32067 mycoplasma	531	1	KCCG_HUMAN	Q9vzu2 deinococcus
465	1.8	462	1	CHI1_CANAL	P32067 mycoplasma	531	1	KCCG_HUMAN	Q9vzu2 deinococcus
466	1.8	462	1	ILGA_MOUSE	P32067 mycoplasma	531	1	KCCG_HUMAN	Q9vzu2 deinococcus
467	1.8	463	1	CTXA_CARAL	Q8zfv7 yersinia pe	532	1	KCCG_HUMAN	Q9vzu2 deinococcus
468	1.8	463	1	CTXA_CARAL	Q8zfv7 yersinia pe	532	1	KCCG_HUMAN	Q9vzu2 deinococcus
469	1.8	466	1	PA7_HUMAN	O60005 bacillus su	534	1	KCCG_HUMAN	Q9vzu2 deinococcus
470	1.8	470	1	T10A_HUMAN	O13724 schizosacch	535	1	KCCG_HUMAN	Q9vzu2 deinococcus
471	1.8	471	1	Y872_HAEIN	P22272 mus musculu	536	1	KCCG_HUMAN	Q9vzu2 deinococcus
					Q57486 haemophilus	537	1	KCCG_HUMAN	Q9vzu2 deinococcus
					P46876 candida alb	538	1	KCCG_HUMAN	Q9vzu2 deinococcus
					P22273 rattus norv	539	1	KCCG_HUMAN	Q9vzu2 deinococcus
					Q9gnn8 carybdea al	540	1	KCCG_HUMAN	Q9vzu2 deinococcus
					P08709 homo sapien	541	1	KCCG_HUMAN	Q9vzu2 deinococcus
					O00220 homo sapien	541	1	KCCG_HUMAN	Q9vzu2 deinococcus
					RAN1_SCHPO	543	1	KCCG_HUMAN	Q9vzu2 deinococcus
					Q57491 haemophilus	544	1	KCCG_HUMAN	Q9vzu2 deinococcus

545	6	1.8	551	1	RN27_HUMAN	Q9b2r9 homo sapien	618	6	1.8	661	1	WHI3_YEAST	P34761 saccharomyc
546	6	1.8	551	1	RN27_MOUSE	Q99qj2 mus musculus	619	6	1.8	665	1	HS70_ECHGR	Q24789 echinococcu
547	6	1.8	552	1	ARRA_ARATH	Q49397 arabidopsis	620	6	1.8	665	1	HS72_HUMAN	Q14807 homo sapien
548	6	1.8	552	1	UB18_XYLFA	Q9pce8 xyella fas	621	6	1.8	667	1	TKT2_ECOLI	P33570 escherichia
549	6	1.8	552	1	UB18_XYLFT	Q87cni xyella fas	622	6	1.8	668	1	TKT_XANFL	P51010 xanthobacte
550	6	1.8	557	1	MAOX_ANAPL	P28227 anas platyr	623	6	1.8	669	1	MM15_HUMAN	P51511 homo sapien
551	6	1.8	557	1	MAOX_COLL1	P40927 columba liv	624	6	1.8	674	1	CIN_DROME	P39205 drosophila
552	6	1.8	557	1	YU61_VIBMA	Q9ral1 vibrio mari	625	6	1.8	674	1	YB66_YEAST	P38315 saccharomyc
553	6	1.8	564	1	ARX_MOUSE	Q35085 mus musculus	626	6	1.8	682	1	E13B_BACCI	P29303 bacillus ci
554	6	1.8	564	1	ASMI_CAEEL	Q10916 caenorhabdi	627	6	1.8	682	1	S219_RAT	Q9jhi3 rattus norv
555	6	1.8	566	1	P11B_PSEAE	P22608 pseudomonas	628	6	1.8	686	1	ATKB_MYXXA	Q93mv5 myxococcus
556	6	1.8	567	1	CYDC_BACSU	P94366 bacillus su	629	6	1.8	690	1	SYGB_EUCAL	P57235 buchnera ap
557	6	1.8	567	1	FZD7_CHICK	Q57329 gallus gall	630	6	1.8	695	1	NU5C_CAPBA	Q31952 capsaicin ba
558	6	1.8	568	1	TAPB_AERHY	P45792 aeromonas h	631	6	1.8	695	1	NU5C_LYCPS	Q32516 lycopersico
559	6	1.8	574	1	ENV_SRV2R	P51520 simian retr	632	6	1.8	702	1	UNOB_PROMI	Q86988 proteus mir
560	6	1.8	574	1	ILD2_BRAJA	Q89xy5 bradyrhizob	633	6	1.8	703	1	COAT_SMSV4	P36285 san miguel
561	6	1.8	576	1	ACH2_DROME	P17644 drosophila	634	6	1.8	704	1	MD22_SCHPO	Q9p7v8 schizosacch
562	6	1.8	576	1	HXY4_YEAST	P32467 saccharomyc	635	6	1.8	707	1	GCVK_HCNVA	P16788 human cytom
563	6	1.8	577	1	ALG8_YEAST	P40351 saccharomyc	636	6	1.8	710	1	PKN6_MYXXA	P54738 myxococcus
564	6	1.8	579	1	PHOR_BACSU	P23545 bacillus su	637	6	1.8	711	1	Z316_HUMAN	Q9h116 homo sapien
565	6	1.8	585	1	DHSA_BACSU	P08065 bacillus su	638	6	1.8	712	1	E2BE_YEAST	P32501 saccharomyc
566	6	1.8	588	1	C166_CHICK	P42292 gallus gall	639	6	1.8	713	1	CADD_HUMAN	P55290 homo sapien
567	6	1.8	590	1	HMPF_DROME	P07548 drosophila	640	6	1.8	715	1	UNVRD_MYCPN	P75437 mycoplasma
568	6	1.8	591	1	FLGE_CAUCR	P35806 caulobacter	641	6	1.8	723	1	DL11_HUMAN	O00548 homo sapien
569	6	1.8	592	1	FTS2_BARBA	Q31314 bartonella	642	6	1.8	725	1	HS9B_BRARE	O57521 brachydanio
570	6	1.8	596	1	GPD2_ARATH	Q9fy99 arabidopsis	643	6	1.8	727	1	PEC1_MOUSE	Q08481 mus musculus
571	6	1.8	597	1	LEPA_VIBVU	Q8dc78 vibrio vuln	644	6	1.8	731	1	DAXX_RAT	Q8vib2 rattus norv
572	6	1.8	600	1	S133_MOUSE	Q91y63 mus musculus	645	6	1.8	731	1	GOA5_HUMAN	Q8tba6 homo sapien
573	6	1.8	600	1	S133_RAT	Q92025 rattus norv	646	6	1.8	735	1	C1GB_DICDI	Q94481 dictyosteli
574	6	1.8	601	1	3BF1_MOUSE	P55194 mus musculus	647	6	1.8	735	1	MCMS_XENLA	P55862 xenopus lae
575	6	1.8	603	1	C4BB_ARATH	Q9zpr1 arabidopsis	648	6	1.8	738	1	DX_DROME	Q23985 drosophila
576	6	1.8	603	1	PURL_THEMEA	Q9x0x3 thermotoga	649	6	1.8	739	1	DAXX_MOUSE	Q35613 mus musculus
577	6	1.8	603	1	YD25_MYCTU	Q10637 mycobacteri	650	6	1.8	740	1	NU5C_TOBAC	P06265 nicotiana t
578	6	1.8	618	1	DNAK_CORGL	Q8nly6 corynebacte	651	6	1.8	743	1	BGAL_THEET	P77989 thermosane
579	6	1.8	619	1	DNAK_COREF	Q8fm78 corynebacte	652	6	1.8	754	1	Z287_HUMAN	Q9hbt7 homo sapien
580	6	1.8	620	1	KHL8_BOVIN	Q9p599 homo sapien	653	6	1.8	759	1	Z287_MOUSE	Q9eqd9 mus musculus
581	6	1.8	620	1	S6A6_BOVIN	Q9mz34 bos taurus	654	6	1.8	761	1	METS_VIBCH	Q9krd8 vibrio chol
582	6	1.8	620	1	S6A6_CANFA	Q00589 canis famil	655	6	1.8	766	1	ICCR_DROME	Q08180 drosophila
583	6	1.8	620	1	S6A6_HUMAN	P31641 homo sapien	656	6	1.8	766	1	GAP1_SCHPO	P33277 schizosacch
584	6	1.8	621	1	LONH_ARCFU	Q29883 archaeoglob	657	6	1.8	767	1	CC10_SCHPO	P01129 schizosacch
585	6	1.8	621	1	S6A6_MOUSE	Q35316 mus musculus	658	6	1.8	772	1	ELA1_HUMAN	Q14241 homo sapien
586	6	1.8	621	1	S6A6_RAT	P31643 rattus norv	659	6	1.8	775	1	POT3_ARATH	Q9fe38 arabidopsis
587	6	1.8	622	1	3BF1_HUMAN	Q9y3l3 homo sapien	660	6	1.8	775	1	REP_BHPF1	P51711 bacteriophag
588	6	1.8	622	1	COX1_BACSU	P24010 bacillus su	661	6	1.8	779	1	MSS4_YEAST	P38994 saccharomyc
589	6	1.8	624	1	COX1_BACPF	Q04440 bacillus ps	662	6	1.8	784	1	LOH_RICPR	Q9zd92 rickettsia
590	6	1.8	625	1	XYNA_PIRSP	Q12667 piromyces s	663	6	1.8	787	1	OBP_HSV7J	P52179 human herpe
591	6	1.8	626	1	RN17_MOUSE	Q99mv7 mus musculus	664	6	1.8	788	1	QOXM_SULAC	P39481 sulfolobus
592	6	1.8	627	1	K2C1_MOUSE	P04104 mus musculus	665	6	1.8	788	1	ARNT_RABIT	O02748 oryctolagus
593	6	1.8	629	1	SKIL_MOUSE	Q60665 mus musculus	666	6	1.8	790	1	DNL1_ARATH	Q42572 arabidopsis
594	6	1.8	630	1	MNT3_YEAST	P40549 saccharomyc	667	6	1.8	796	1	SEC6_CAEEL	Q19262 caenorhabdi
595	6	1.8	632	1	APS_HUMAN	Q14492 homo sapien	668	6	1.8	800	1	GUN_BACS1	P06564 bacillus ep
596	6	1.8	634	1	GLGB_LACPL	Q89011 lactobacill	669	6	1.8	801	1	SC34_YEAST	P40094 saccharomyc
597	6	1.8	636	1	YNR6_YEAST	P53882 saccharomyc	670	6	1.8	801	1	VPS_RDVA	P14583 rice dwarf
598	6	1.8	637	1	FTSH_BACSU	P37476 bacillus su	671	6	1.8	801	1	VPS_RDVF	Q85437 rice dwarf
599	6	1.8	640	1	C5P1_ARATH	Q8h0v1 arabidopsis	672	6	1.8	803	1	SYFB_WIGBR	Q8d3b5 wiggleswort
600	6	1.8	640	1	HS7A_CAEEL	P09446 caenorhabdi	673	6	1.8	804	1	DPF6_MOUSE	Q94218 mus musculus
601	6	1.8	640	1	HS7C_DICDI	P36415 dictyosteli	674	6	1.8	804	1	YBBP_ECOLI	P77504 escherichia
602	6	1.8	641	1	NUSM_ALLMA	Q30365 allomyces m	675	6	1.8	809	1	AL14_SCHPO	Q94534 schizosacch
603	6	1.8	641	1	UGS2_SOLTU	P93568 solanum tub	676	6	1.8	812	1	LOH_BRUAB	O52605 bruceella ab
604	6	1.8	643	1	HS71_SCHPO	Q10265 schizosacch	677	6	1.8	812	1	LOH_BRUME	Q8ync6 bruceella me
605	6	1.8	643	1	Y903_METJA	Q58313 methanococc	678	6	1.8	812	1	LOH_BRUSE	Q89017 bruceella su
606	6	1.8	644	1	LOH1_METTH	Q26878 methanobact	679	6	1.8	819	1	AD05_HUMAN	P13414 homo sapien
607	6	1.8	648	1	S281_RAT	Q62674 rattus norv	680	6	1.8	828	1	PMFC_PROMI	P35514 proteus mir
608	6	1.8	649	1	HS70_PYRSA	P37899 pyrenomonas	681	6	1.8	828	1	YKR6_YEAST	P34239 saccharomyc
609	6	1.8	650	1	AMPB_HUMAN	Q9h4a4 homo sapien	682	6	1.8	829	1	SC10_ARATH	Q8rvq5 arabidopsis
610	6	1.8	650	1	Y096_MYCGE	P97342 mycoplasma	683	6	1.8	830	1	SREC_HUMAN	Q14162 homo sapien
611	6	1.8	652	1	HS70_LEIAM	Q07437 leishmania	684	6	1.8	836	1	GCS1_HUMAN	Q13724 homo sapien
612	6	1.8	653	1	HS70_LEIDO	P17804 leishmania	685	6	1.8	842	1	ABC6_HUMAN	Q9np58 homo sapien
613	6	1.8	653	1	RN17_HUMAN	Q9bxt8 homo sapien	686	6	1.8	848	1	TOP1_BORBU	O51768 borrelia bu
614	6	1.8	654	1	HS70_HYDMA	Q05944 hydra magni	687	6	1.8	851	1	YKM1_YEAST	P32330 saccharomyc
615	6	1.8	654	1	YLH4_SCHPO	Q9hgq2 schizosacch	688	6	1.8	855	1	CNRC_BOVIN	P16586 bos taurus
616	6	1.8	657	1	MM15_MOUSE	O54732 mus musculus	689	6	1.8	856	1	AAP1_YEAST	P37898 saccharomyc
617	6	1.8	661	1	HS74_TRYBB	P11145 trypanosoma	690	6	1.8	858	1	POT7_ARATH	Q9fy75 arabidopsis

FT PROPEP 25 29 BY SIMILARITY.
 FT CHAIN 30 669 BETA-GALACTOSIDASE.
 FT ACT SITE 189 199 PROTON DONOR (BY SIMILARITY).
 FT ACT SITE 269 269 NUCLEOPHILE (POTENTIAL).
 FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 547 547 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 557 557 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 483 483 R -> P (IN REF. 2).
 SQ SEQUENCE 669 AA; 75229 MW; 35864933B5E2F76 CRC64;

Query Match 2.4%; Score 8; DB 1; Length 669;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLLL 238
 DB 12 LLLVPLLL 19
 |||||

RESULT 3
 ID DSG2 HUMAN STANDARD; PRT; 1117 AA.
 AC Q14126;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Desmoglein 2 precursor (HDGC).
 GN DSG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=94192736; PubMed=8143788;
 RA Schaefer S.; Koch P.J.; Franke W.W.;
 RT "Identification of the ubiquitous human desmoglein, Dsg2, and the
 RT expression catalogue of the desmoglein subfamily of desmosomal
 RT cadherins.";
 RL Exp. Cell Res. 211:391-399(1994).
 RN [2]
 RP SEQUENCE OF 777-1117 FROM N.A.
 RX MEDLINE=92037656; PubMed=1935985;
 RA Koch P.J.; Goldschmidt M.D.; Walsh M.J.; Zimbelmann R.; Franke W.W.;
 RT "Complete amino acid sequence of the epidermal desmoglein precursor
 RT polypeptide and identification of a second type of desmoglein gene.";
 RL Eur. J. Cell Biol. 55:200-208(1991).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITE ASN-111.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H.; Li X.-J.; Martin D.B.; Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 CC -!- FUNCTION: Component of intercellular desmosome junctions. Involved
 CC in the interaction of plaque proteins and intermediate filaments
 CC mediating cell-cell adhesion.
 CC -!- SUBCELLULAR LOCATION: Type I transmembrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: All of the tissues tested and carcinomas.
 CC -!- DOMAIN: Calcium may be bound by the cadherin-like repeats
 CC (Potential).
 CC -!- SIMILARITY: Contains 4 cadherin domains.

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CC or send an email to license@isb-sib.ch).
 DR EMBL; Z26317; CA81226.1; -.
 DR PIR; S38673; S38673.
 DR HSSP; P15116; INCI.
 DR Genew; HGNC:3049; DSG2.
 DR MIM; 125671; -.
 DR GO; GO:0005911; C:intercellular junction; TAS.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; cadherin; 4.
 DR PRINTS; PR00205; CADHERIN.
 DR SMART; SMO0112; CA; 4.
 DR PROSITE; PS00232; CADHERIN 1; 3.
 DR PROSITE; PS0268; CADHERIN 2; 4.
 KW Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
 KW Cytoskeleton; Calcium-binding.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 48 POTENTIAL.
 FT CHAIN 49 1117 DESMOGLEIN 2.
 FT DOMAIN 49 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 633 POTENTIAL.
 FT DOMAIN 634 1117 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 49 159 CADHERIN 1.
 FT DOMAIN 160 272 CADHERIN 2.
 FT DOMAIN 273 387 CADHERIN 3.
 FT DOMAIN 388 502 CADHERIN 4.
 FT REPEAT 880 911 DESMOGLEIN REPEAT 1.
 FT REPEAT 912 941 DESMOGLEIN REPEAT 2.
 FT REPEAT 942 967 DESMOGLEIN REPEAT 3.
 FT REPEAT 968 991 DESMOGLEIN REPEAT 4.
 FT REPEAT 992 1020 DESMOGLEIN REPEAT 5.
 FT REPEAT 1021 1050 DESMOGLEIN REPEAT 6.
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1117 AA; 122385 MW; 223B897FED70B289 CRC64;

Query Match 2.4%; Score 8; DB 1; Length 1117;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLLL 238
 DB 624 LLLVPLLL 631
 |||||

RESULT 4
 ID DSG2 MOUSE STANDARD; PRT; 1122 AA.
 AC O5511; O8K069; Q8R517;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Desmoglein 2 precursor.
 GN DSG2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Zhuxiang N.; Garrod D.R.;
 RT "Desmosomal cadherins mediate homophilic cell adhesion.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP SEQUENCE OF 348-1122 FROM N.A.
 RC STRAIN=CS2BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3].
RP SEQUENCE OF i042-1122 FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=9067789; PubMed=9404003;
RA King I.A., Angst B.D., Hunt D.M., Kruger M., Arnemann J., Buxton R.S.;
RT "Hierarchical expression of desmosomal cadherins during stratified
RT epithelial morphogenesis in the mouse";
RL Differentiation 62:83-96(1997).
CC -1- FUNCTION: Component of intercellular desmosome junctions. Involved
CC in the interaction of plaque proteins and intermediate filaments
CC mediating cell-cell adhesion.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed uniformly in all E12.5 epithelia,
CC gradually becoming confined to the basal cell layers during
CC epithelial stratification.
CC -1- DOMAIN: Calcium may be bound by the cadherin-like repeats
CC (potential).
CC -1- SIMILARITY: Contains 4 cadherin domains.
CC
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CC
CC EMBL; AB072269; BAB86843.1; -;
CC EMBL; BC034056; AAH34056.1; -;
CC EMBL; AJ000328; CAA03995.1; -;
CC MGD; MGI:1196466; Dsg2.
CC GO; GO:0030057; C:desmosome; IDA.
CC InterPro; IPR002126; Cadherin.
CC Pfam; PF00028; cadherin; 4.
CC PRINTS; PR00205; CADHERIN.
CC SMART; SM00112; CA; 4.
CC PROSITE; PS00232; CADHERIN_1; 3.
CC PROSITE; PS0268; CADHERIN_2; 4.
CC Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal;
KW Cytoskeleton; Calcium-binding.
FT SIGNAL 1 28 POTENTIAL.
FT PROPEP 29 54 POTENTIAL.
FT CHAIN 25 1122 DESMOGLEIN 2.
FT DOMAIN 29 618 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 619 639 POTENTIAL.
FT DOMAIN 640 1122 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 54 164 CADHERIN 1.
FT DOMAIN 165 277 CADHERIN 2.
FT DOMAIN 278 398 CADHERIN 3.
FT DOMAIN 397 504 CADHERIN 4.
FT REPEAT 885 916 DESMOGLEIN REPEAT 1.
FT REPEAT 917 945 DESMOGLEIN REPEAT 2.
FT REPEAT 946 971 DESMOGLEIN REPEAT 3.
FT REPEAT 972 995 DESMOGLEIN REPEAT 4.
FT REPEAT 996 1024 DESMOGLEIN REPEAT 5.
FT REPEAT 1025 1055 DESMOGLEIN REPEAT 6.

FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 358 358 I -> L (IN REF. 2).
FT CONFLICT 480 480 E -> D (IN REF. 2).
FT CONFLICT 491 491 V -> I (IN REF. 2).
FT CONFLICT 863 863 T -> R (IN REF. 2).
FT CONFLICT 899 899 R -> H (IN REF. 2).
SQ SEQUENCE 1122 AA; 122397 MW; CECOC489F858ED57 CRC64;
Query Match 2.4%; Score 8; DB 1; Length 1122;
Best Local Similarity 100.08; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 231 LLLVPLLL 238
DB 630 LLLVPLLL 637
RESULT 5
MTRF METKA
ID MTRF METKA STANDARD; PRT; 75 AA.
AC Q8TVA7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Tetrahydromethanopterin S-methyltransferase subunit F (EC 2.1.1.86)
DE (NS-methyltetrahydromethanopterin--coenzyme M methyltransferase
DE subunit F).
GN MTRF OR MK1485.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -1- FUNCTION: Part of a complex that catalyzes the formation of
CC methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
CC sodium-ion translocating step (By similarity).
CC -1- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
CC (methylthio)ethanesulfonate.
CC -1- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
CC -1- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC,
CC mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane-anchored (potential).
CC -1- MISCELLANEOUS: Unlike other orthologs, mtrF from M.kandleri is not
CC located in the mtr operon.
CC -1- SIMILARITY: Belongs to the mtrF family.
CC
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CC
CC EMBL; AE010439; AA002698.1; -;
CC HAMAP; MF_01099; -; 1.
KW Methanogenesis; One-carbon metabolism; Transferase; Methyltransferase;
KW Transmembrane; Complete proteome.

FT TRANSMEM 53 73 POTENTIAL.
SQ SEQUENCE 75 AA; 8130 MW; 0186C402CCFCE28 CRC64;

Query Match 2.1%; Score 7; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 LLVPLLL 238
| | | | |
DB 66 LLVPLLL 72

RESULT 6
SY08_MOUSE
ID SY08_MOUSE STANDARD; PRT; 97 AA.
AC Q92131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemoattractant protein 2).
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN CCL8 OR SCYA8 OR MCP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Nomiya H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gofjoberi T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gascerland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RL Nature 409:685-690(2001).
RT "Functional annotation of a full-length mouse cDNA collection.";
CC CC
CC -1- FUNCTION: Chemotactic factor that attracts monocytes. This protein can bind heparin (By similarity).
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC
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CC
CC EMBL; AB023418; BAA75014.1; -;
CC EMBL; AK007942; BAB25365.1; -;
CC HSSP; P51671; 1E0T.
CC MGD; MGI:101878; Ccl8.
CC InterPro; IPR000827; CC_chemokine_sml.
CC InterPro; IPR001811; Chemokine_IL8.

DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; FALSE_NEG.
KW Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 97 SMALL INDUCIBLE CYTOKINE A8.
FT DISULFID 32 57 BY SIMILARITY.
FT DISULFID 33 73 BY SIMILARITY.
SQ SEQUENCE 97 AA; 11017 MW; 65BB3722F3F98D54 CRC64;

Query Match 2.1%; Score 7; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VLLCLLL 233
| | | | |
DB 6 VLLCLLL 12

RESULT 7
SV13_HUMAN
ID SV13_HUMAN STANDARD; PRT; 98 AA.
AC Q99616; O95689;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Small inducible cytokine A13 precursor (CCL13) (Monocyte chemoattractant protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CK-beta-10) (NCC-11).
DE CCL13 OR SCYA13 OR MCP4 OR NCCL1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=97111354; PubMed=8955214;
RA Garcia-Zepeda E.A., Combadiere C., Rothenberg M.E., Sarafi M.N.,
RA Lavigne F., Hamid Q., Murphy P.M., Luster A.D.;
RT "Human monocyte chemoattractant protein (MCP)-4 is a novel CC chemokine with activities on monocytes, eosinophils, and basophils induced in allergic and nonallergic inflammation that signals through the CC chemokine receptors (CCR)-2 and -3.";
RL J. Immunol. 157:5613-5626(1996).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
RC TISSUE=Fetal;
RX MEDLINE=96235049; PubMed=8642349;
RA Ugucioni M., Loutscher P., Forsemann U., Dewald B., Li H., Lima S.H.,
RA Li Y., Kreider B., Garotta G., Thelen M., Baggiolini M.;
RT "Monocyte chemoattractant protein 4 (MCP-4), a novel structural and functional analogue of MCP-3 and eotaxin.";
RL J. Exp. Med. 183:2379-2384(1996).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
RC TISSUE=Fetal;
RX MEDLINE=97341179; PubMed=9195948;
RA Berkhout T.A., Sarau H.M., Moores K., White J.R., Elshourbagy N.,
RA Appelbaum E., Respe T.J., Brawner M., Makwana J., Foley J.J.,
RA Schmidt D.B., Imburgia C., Macnulty D., Matthews J., O'Donnell K.,
RA O'Shannessy D., Scott M., Groot P.H.E., Macphee C.;
RT "Cloning, in vitro expression, and functional characterization of a novel human CC chemokine of the monocyte chemoattractant protein (MCP) family (MCP-4) that binds and signals through the CC chemokine receptor 2B.";
RL J. Biol. Chem. 272:16404-16413(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Dante M., Gibson A.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
RA Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=97213770; PubMed=9060459;
RA Godiska R., Chantray D., Raport C.J., Schweickart V.L., Trong H.L.,
RA Gray P.W.;
RT "Monocyte chemotactic protein-4: tissue-specific expression and
RT signaling through CC chemokine receptor-2";
RL J. Leukoc. Biol. 61:353-360(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin fibroblast;
RA MEDLINE=99160888; PubMed=10049733;
RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
RA Bartels J.;
RT "Genomic organization, sequence analysis and transcriptional
RT regulation of the human MCP-4 chemokine gene (SCVA13) in dermal
RT fibroblasts: a comparison to other eosinophilic beta-chemokines";
RL Biochem. Biophys. Res. Commun. 255:470-476(1999).
RN [8]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalios D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 17-95 FROM N.A.
RC TISSUE=Foreskin;
RA Bartels J.H., Schlueter C., Richter E., Noso N., Christophers E.,
RA Schroeder J.-M.;
RT "Expression of a MCP-4 like novel CC-chemokine in human dermal
RT fibroblasts: molecular cloning and RT-PCR analysis";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes,
CC eosinophils and eosinophils, but not neutrophils. Signals through
CC CCR2B and CCR3 receptors. Plays a role in the accumulation of
CC leukocytes at both sides of allergic and nonallergic inflammation.
CC May be involved in the recruitment of monocytes into the arterial
CC wall during the disease process of atherosclerosis. May play a
CC role in the monocyte attraction in tissues chronically exposed to
CC exogenous pathogens.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Widely expressed. Found in small intestine,
CC thymus, colon, lung, trachea, stomach and lymph node. Low levels
CC seen in the pulmonary artery smooth muscle cells.
CC -1- INDUCTION: By interleukin-1 and TNF-alpha.
CC -1- PTM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (LA)MCP-4 AND
CC (LQ)MCP-4 ARE PRODUCED BY DIFFERENTIAL SIGNAL CLEAVAGE.
CC -1- MASS SPECTROMETRY: MW=9314; MW ERR=30; METHOD=MALDI; RANGE=17-98.
CC -1- MASS SPECTROMETRY: MW=8760; MW ERR=30; METHOD=MALDI; RANGE=22-98.
CC -1- MASS SPECTROMETRY: MW=8575; MW ERR=30; METHOD=MALDI; RANGE=24-98.
CC -1- MISCELLANEOUS: This protein can bind heparin.

CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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CC -----
CC EMBL: U46767; AAB38703.1; -;
CC EMBL: AC002482; AAB67307.1; -;
CC EMBL: X98306; CAA66950.1; -;
CC EMBL: U59808; AAD09362.1; -;
CC EMBL: AJ001634; CAA04888.1; -;
CC EMBL: BC008621; AAO08621.1; -;
CC EMBL: 277650; CAB01111.1; -;
CC HSSP: P51671; LEOT.
CC Genew; HGNC:10611; CCL13.
CC MIM: 601391; -;
CC GO: GO:0005615; C:extracellular space; TAS.
CC GO: GO:0008009; F:chemokine activity; TAS.
CC GO: GO:0005102; P:receptor binding; TAS.
CC GO: GO:0006874; P:calcium ion homeostasis; TAS.
CC GO: GO:0007267; P:cell-cell signaling; TAS.
CC GO: GO:0006935; P:chemotaxis; TAS.
CC GO: GO:0006954; P:inflammatory response; TAS.
CC GO: GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR001811; Chemokine IIL8.
CC InterPro; IPR008097; Fractalkine.
CC Pfam; PF00048; IL8; 1.
CC PRINTS; PR01721; FRACTALKINE.
CC SMART; SM00199; SCV; 1.
CC PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CC Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
CC Pyrolydione carboxylic acid.
CC SIGNAL 1 16
CC CHAIN 17 98 SMALL INDUCIBLE CYTOKINE A13, LONG FORM.
CC CHAIN 24 98 SMALL INDUCIBLE CYTOKINE A13, SHORT FORM.
CC MOD RES 24 24 PYROLYDIONE CARBOXYLIC ACID.
CC DISULFID 34 58 BY SIMILARITY.
CC DISULFID 35 74 BY SIMILARITY.
CC CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CONFLICT 93 98 AHTLKT -> LTP (IN REF. 9).
CC SEQUENCE 98 AA; 10986 MW; 612688DFCD308873 CRC64;
Query Match 2.1%; Score 7; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 227 VLLCLLL 233
Db 6 VLLCLLL 12
RESULT 8
RLIX_SPOFR
ID_RLIX_SPOFR STANDARD; PRT; 177 AA.
AC QWQI7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 60S ribosomal protein L18a.
GN RPL18A.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Amphipyrinae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RA Landais I., Ogliastro M., Mita K., Nohata J., Lopez-Ferber M.,

RA Duonor-Cerutti M., Fournier P., Devauchelle G.;
RT "Full-length ribosomal protein sequence from an EST library of
RT *Spodoptera frugiperda* cells (Sf9).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC
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CC
CC EMBL; AY072289; AAL62470.1; -
DR InterPro; IPR002670; Ribosomal_L18ae.
DR Pfam; PF01775; Ribosomal_L18ae; 1.
KW Ribosomal protein.
SQ SEQUENCE 177 AA; 20992 MW; 93D2F8517A5DD0D14 CRC64;

Query Match 2.1%; Score 7; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 SVGGAVT 38
|||
Db 101 SVGGAVT 107

RESULT 9
MURB_BACLI STANDARD; PRT; 184 AA.
ID Q45305;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE acetylmuramate dehydrogenase) (Fragment).
GN MURB.
OS *Bacillus licheniformis*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5A2;
RX MEDLINE=94374713; PubMed=8088553;
RA Harry E.J., Partridge S.R., Weiss A.S., Wake R.G.;
RT "Conservation of the 16S divB gene in *Bacillus subtilis* W23 and B.
RT *licheniformis*, and evidence for homology to *ftsQ* of *Escherichia*
RT *coli*.";
RL Gene 147:85-89 (1994).
CC
CC -!- FUNCTION: Cell wall formation (BY similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC
CC -!- COFACTOR: FAD.
CC
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC
CC -!- SIMILARITY: Belongs to the murB family.
CC
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CC
CC EMBL; U01958; AAA57244.1; -
DR DR PIR; I40220; 140220.
DR HSSP; P08373; 2MBR.
DR HMAP; MF_00037; -; 1.
DR InterPro; IPR003170; MurB.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD_binding_4; 1.

DR Pfam; PF02873; MurB_C; 1.
KW Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;
KW NADP; Flavoprotein; FAD.
FT NON_TER 1
SQ SEQUENCE 184 AA; 20166 MW; 4114D8B29AE21EFD CRC64;

Query Match 2.1%; Score 7; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGGAV 37
|||
Db 9 GSVGGAV 15

RESULT 10
YD48_AQUAE STANDARD; PRT; 189 AA.
ID YD48_AQUAE
AC Q67363;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1348.
GN AQ_1348.
OS *Aquifex aeolicus*.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VFS;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Auja M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium *Aquifex*
RT *aeolicus*.";
RL Nature 392:353-358 (1998).
CC
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CC
CC EMBL; AE000736; AAC07334.1; -
DR DR PIR; H70416; H70416.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 189 AA; 21788 MW; A70F714263221FFE CRC64;

Query Match 2.1%; Score 7; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 GLFLMFL 250
|||
Db 142 GLFLMFL 148

RESULT 11
UT11_ARATH STANDARD; PRT; 228 AA.
ID UT11_ARATH
AC Q9M223;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable U3 small nuclear RNA-associated protein 11 (U3 snRNA-
DE associated protein 11).
GN AT3G60360 OR T8B10.20.
OS *Arabidopsis thaliana* (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=1130713;
RA Salanoubat M., Lemcke K., Rieger H., Perez-Alonso M., Obermaier B.,
RA Fartmann B., Valle G., Bloeker H., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone P., Choigne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Catolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Sminionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casasuberta E.,
RA Monfort A., Argirou A., Flores M., Liquori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rued S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idegawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RN Nature 408:820-822(2000).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.B., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.P.,
RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamoe R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.,
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RN Science 302:842-846(2003).
RL [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troughan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.,
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in nucleolar processing of pre-18S ribosomal
CC RNA (By similarity).
CC -!- SUBUNIT: Component of the ribosomal small subunit (SSU)
CC processome (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear;
CC -!- SIMILARITY: Belongs to the UTP11 family.
CC
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DR EMBL; AL138646; CAB81822.1; -
DR EMBL; AY039876; AAK63980.1; -
DR EMBL; AY101514; AAM26635.1; -
DR EMBL; BT000725; AAN31867.1; -
DR EMBL; AY085156; AAM61709.1; -
DR FIR; T47847; T47847.
DR InterPro; IPR007144; Utp11.
DR Pfam; PF03998; Utp11.1.
KW rRNA processing; Nuclear protein.
SQ SEQUENCE 228 AA; 27149 MW; DF6DB3112383CB5A CRC64;

Query Match 2.1%; Score 7; DB 1; Length 228;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 STVEIPK 311
DB 155 STVEIPK 161
|||||
|

RESULT 12
YTML_BACSU
ID YTML_BACSU STANDARD; PRT; 239 AA.
AC 034315;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable amino-acid ABC transporter permease protein ytmL.
GN YTML OR BSU29360.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98048467; PubMed=9387221;
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
RT in the 200 kb rnb-dnaB region.";
RL Microbiology 143:3431-3441(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conner I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haelegh J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Schleich S., Schroeter R., Sadia Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Takatoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambut R., Wedler H., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.";
 RL Nature 390:249-256(1997).
 CC -!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM YTMKLN FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR THE
 CC TRANSLLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
 CC system permease family. HisMQ subfamily.
 CC -----
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 CC -----
 DR EMBL; AF008220; AAC00327.1; -;
 DR EMBL; Z99118; CAB14896.1; -;
 DR PIR; F69996; F69996.
 DR Subtilist; BG13886; ytmL.
 DR InterPro; IPR000515; BPD_transp.
 DR Pfam; PF00528; BPD_transp; 1.
 DR PROSITE; PS0928; ABC_TM1; 1.
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane;
 FT Complete proteome.
 KW TRANSMEM 25 45 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 196 216 POTENTIAL.
 SQ SEQUENCE 239 AA; 26239 MW; AE0D17AC254D6239 CRC64;
 Query Match 2.1%; Score 7; DB 1; Length 239;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 FVLGLFL 247
 DB 36 FVLGLFL 42
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 RESULT 13
 ID FLIP CAUCR STANDARD; PRT; 266 AA.
 AC Q45980;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Flagellar biosynthetic protein flip.
 GN FLIP OR CC0951.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=95325304; PubMed=7601928;
 RA Guber J.W., Boyd C.H., Jarvis M., Mangan E.K., Rizzo M.F.,
 RA Wingrove J.A.;
 RT "Temporal and spatial regulation of flip, an early flagellar gene of
 RT Caulobacter crescentus that is required for motility and normal cell
 RT division.";
 RL J. Bacteriol. 177:3656-3667(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 CC -!- FUNCTION: MAY BE A COMPONENT OF THE FLAGELLUM. IT IS REQUIRED FOR
 CC NORMAL CELL DIVISION. MAY BE IMPLICATED IN THE SECRETION OF
 CC VIRULENCE FACTORS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
 CC -----
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 DR EMBL; U20387; AAA86882.1; -;
 DR EMBL; AE005772; AAK22935.1; -;
 DR PIR; C87387; C87387.
 DR TIGR; CC0951; -;
 DR InterPro; IPR005837; Flip.
 DR InterPro; IPR005838; TypeIII_P.
 DR Pfam; PF00813; Flip; 1.
 DR PRINTS; PR01302; TYPE3IMPPROT.
 DR PRODOM; PD002586; TypeIII_P; 1.
 DR TIGRFAMs; TIGR01103; Flip_1; 1.
 DR PROSITE; PS01060; Flip_1; 1.
 DR PROSITE; PS01061; Flip_2; 1.
 KW Flagellum; Transmembrane; Complete proteome.
 FT TRANSMEM 20 40 POTENTIAL.
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 102 122 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 SQ SEQUENCE 266 AA; 28537 MW; A84F17CB1C65A947 CRC64;
 Query Match 2.1%; Score 7; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 21 AASGPVK 27
 DB 146 AASGPVK 152
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 RESULT 14
 ID CFQX GUITH STANDARD; PRT; 293 AA.
 AC Q78450;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CfxQ protein homolog.
 GN CFQX.
 OS Guillardia theta (Cryptomonas phi).
 OG Chloroplast.
 OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
 OX NCBI_TaxID=55529;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99128221; PubMed=9929392;
 RA Douglas S.E., Penny S.L.;
 RT "The plastid genome of the cryptophyte alga, *Guillardia theta*:
 RT complete sequence and conserved syntenic groups confirm its common
 RT ancestry with red algae.";
 RL J. Mol. Evol. 48:236-244(1999).
 CC -!- FUNCTION: Necessary for the expression of RuBisCO (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast.
 CC -!- SIMILARITY: BELONGS TO THE CBXX/CFQX FAMILY.

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DR EMBL; AF041468; AAC35641.1; -
DR InterPro; IPR003593; AAA_Apase.
DR InterPro; IPR003959; AAA_Apase_Centr.
DR InterPro; IPR000641; CBX_Cfg.
DR Pfam; PF00004; AAA; 1.
DR PRINTS; PR00819; CBXCFQXUPER.
DR SMART; SM00382; AAA; 1.
DR ATP-binding; Chloroplast.
FT NP BIND 72 79 ATP (POTENTIAL).
SQ SEQUENCE 293 AA; 33560 MW; 7F7476B7EC34915 CRC64;

Query Match 2.1%; Score 7; DB 1; Length 293;
Best Local Similarity 100.0%; Pred.No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 LVTIQPE 66
Db 277 LVTIQPE 283
|||||

RESULT 15
MURB STRA3 : STANDARD; PRT; 300 AA.
ID QBE53; Q8DZ19;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylglucosaminylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE acetylglucosamine dehydrogenase).
GN MURB OR GBS1179 OR SAG112.
OS Streptococcus agalactiae (serotype III), and
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495, 216466;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
RA Meadek T., Zouine M., Couve E., Lalioui L., Poyart C., Tieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease."
RL Mol. Microbiol. 45:1499-1513 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Kouri H., Mulligan K.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli I., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
CC -!- FUNCTION: Cell wall formation (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.

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CC -!- COFACTOR: FAD (By similarity).
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murB family.
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DR EMBL; AL766849; CAD46838.1; -
DR EMBL; AE014242; AAM99993.1; -
DR Sagalib; gbs1179; -
DR TIGR; SAG1112; -
DR HAMAP; MF_00037; -; 1.
DR InterPro; IPR003170; MurB.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD binding_4; 1.
DR Pfam; PF02873; MurB_C; 1.
DR Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
KW Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 300 AA; 32978 MW; 3FCC5590FBF2ED97 CRC64;

Query Match 2.1%; Score 7; DB 1; Length 300;
Best Local Similarity 100.0%; Pred.No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GSVGAV 37
Db 125 GSVGAV 131
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Search completed: August 18, 2004, 15:59:39
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:42:01 ; Search time 19 Seconds
(without alignments)
910.247 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPTCLTLYILWLTGS.....PHSLTMDPTPLPAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pep:*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/2/iaa/PTUS COMB.pep:*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	362.5	20.5	329	4	US-09-149-476-483
2	186	10.5	343	1	US-08-348-792-10
3	186	10.5	343	2	US-08-462-738-10
4	186	10.5	343	4	US-09-199-955-10
5	186	10.5	343	4	US-08-880-875-10
6	182.5	10.3	335	1	US-08-348-792-2
7	182.5	10.3	335	2	US-08-462-738-2
8	182.5	10.3	335	4	US-09-199-955-2
9	182.5	10.3	335	4	US-08-880-875-2
10	182.5	10.3	335	4	US-09-369-248A-3
11	180	10.2	307	1	US-08-348-792-8
12	180	10.2	307	2	US-08-462-738-8
13	180	10.2	307	4	US-09-199-955-8
14	180	10.2	307	4	US-08-880-875-8
15	164.5	9.3	305	1	US-08-348-792-6
16	164.5	9.3	305	2	US-08-462-738-6
17	164.5	9.3	305	4	US-09-199-955-6
18	164.5	9.3	305	4	US-08-880-875-6
19	158.5	8.9	329	1	US-08-348-792-12
20	158.5	8.9	329	2	US-08-462-738-12
21	158.5	8.9	329	4	US-09-199-955-12
22	158.5	8.9	329	4	US-08-880-875-12
23	152	8.6	298	1	US-08-348-792-4
24	152	8.6	298	2	US-08-462-738-4
25	152	8.6	298	4	US-09-199-955-4
26	152	8.6	298	4	US-08-880-875-4
27	150.5	8.5	285	4	US-09-369-248A-2

28	141	8.0	149	4	US-09-227-357-443	Sequence 443, App
29	140.5	7.9	143	4	US-09-227-357-192	Sequence 192, App
30	136.5	7.7	351	3	US-08-466-465-6	Sequence 6, Appl
31	128	7.2	225	1	US-08-328-152A-31	Sequence 31, Appl
32	128	7.2	321	6	US-08-328-152A-31	Patent No. 5169835
33	125.5	7.1	464	2	US-08-602-725-32	Sequence 32, Appl
34	123	6.9	199	1	US-08-328-152A-36	Sequence 36, Appl
35	119.5	6.7	365	3	US-08-979-424-3	Sequence 3, Appl
36	119.5	6.7	365	3	US-09-272-496-2	Sequence 2, Appl
37	119.5	6.7	418	3	US-08-630-172-18	Sequence 18, Appl
38	119.5	6.7	418	3	US-09-375-419-18	Sequence 18, Appl
39	117.5	6.6	344	2	US-08-602-725-34	Sequence 34, Appl
40	117.5	6.6	365	3	US-08-928-383B-2	Sequence 2, Appl
41	116.5	6.6	319	1	US-08-597-495B-22	Sequence 22, Appl
42	116.5	6.6	319	3	US-09-068-051A-2	Sequence 22, Appl
43	116.5	6.6	319	4	US-09-336-536-67	Sequence 67, Appl
44	116.5	6.6	319	4	US-09-254-465A-6	Sequence 6, Appl
45	115.5	6.5	184	3	US-08-630-172-2	Sequence 2, Appl
46	115.5	6.5	184	3	US-09-375-419-2	Sequence 2, Appl
47	114.5	6.5	642	1	US-08-217-299-1	Sequence 1, Appl
48	114.5	6.5	698	2	US-08-602-725-36	Sequence 36, Appl
49	114.5	6.5	734	2	US-08-389-459A-17	Sequence 17, Appl
50	114.5	6.5	734	2	US-08-987-867A-17	Sequence 17, Appl
51	111.5	6.3	174	2	US-08-765-536-2	Sequence 2, Appl
52	111.5	6.3	174	5	PCT-US95-08401-2	Sequence 2, Appl
53	109.5	6.2	315	4	US-09-910-174B-28	Sequence 28, Appl
54	109.5	6.2	315	4	US-09-620-461-28	Sequence 28, Appl
55	109	6.2	324	4	US-09-910-174B-6	Sequence 6, Appl
56	109	6.2	324	4	US-09-620-461-6	Sequence 6, Appl
57	105.5	6.0	323	4	US-09-651-200-21	Sequence 21, Appl
58	105.5	6.0	323	5	PCT-US94-09642-2	Sequence 2, Appl
59	105.5	6.0	329	2	US-08-456-104-2	Sequence 2, Appl
60	105.5	6.0	329	2	US-08-101-624-2	Sequence 2, Appl
61	105.5	6.0	329	3	US-08-479-744A-2	Sequence 2, Appl
62	105.5	6.0	329	3	US-08-280-757B-2	Sequence 2, Appl
63	105.5	6.0	329	3	US-08-203-697A-23	Sequence 23, Appl
64	105.5	6.0	329	3	US-08-703-525-23	Sequence 23, Appl
65	105.5	6.0	329	4	US-08-403-253A-4	Sequence 4, Appl
66	105.5	6.0	329	4	US-08-435-816A-4	Sequence 4, Appl
67	105.5	6.0	329	4	US-09-425-762-2	Sequence 2, Appl
68	105.5	6.0	329	4	US-09-837-867A-23	Sequence 23, Appl
69	105.5	6.0	329	5	PCT-US95-02576-23	Sequence 23, Appl
70	104.5	5.9	329	4	US-09-667-135-32	Sequence 32, Appl
71	101.5	5.7	270	4	US-09-254-465A-24	Sequence 24, Appl
72	101.5	5.7	273	4	US-09-254-465A-26	Sequence 26, Appl
73	100.5	5.7	638	4	US-09-228-986-74	Sequence 74, Appl
74	100	5.6	365	3	US-08-928-383B-24	Sequence 24, Appl
75	98.5	5.6	365	3	US-08-928-383B-23	Sequence 23, Appl
76	98	5.5	503	4	US-08-999-689A-6	Sequence 6, Appl
77	97	5.5	773	3	US-08-434-000A-2	Sequence 2, Appl
78	97	5.5	773	3	US-09-313-157-2	Sequence 2, Appl
79	96.5	5.4	534	4	US-09-651-200-6	Sequence 6, Appl
80	96.5	5.4	534	4	US-09-651-200-24	Sequence 24, Appl
81	96	5.4	340	4	US-09-651-200-2	Sequence 2, Appl
82	96	5.4	441	4	US-09-651-200-4	Sequence 4, Appl
83	96	5.4	526	4	US-09-910-174B-9	Sequence 9, Appl
84	96	5.4	526	4	US-09-620-461-9	Sequence 9, Appl
85	95.5	5.4	365	3	US-08-928-383B-26	Sequence 26, Appl
86	95.5	5.4	771	3	US-08-434-000A-8	Sequence 8, Appl
87	95.5	5.4	771	4	US-09-313-157-8	Sequence 8, Appl
88	93.5	5.3	299	3	US-09-188-930-189	Sequence 189, App
89	93.5	5.3	2409	6	5180808-2	Patent No. 5180808
90	93	5.2	316	4	US-09-910-174B-24	Sequence 24, Appl
91	93	5.2	316	4	US-09-620-461-24	Sequence 24, Appl
92	93	5.2	561	3	US-09-192-545-2	Sequence 2, Appl
93	92.5	5.2	299	3	US-09-188-930-331	Sequence 331, App
94	92.5	5.2	299	4	US-09-462-270-2	Sequence 2, Appl
95	92.5	5.2	299	4	US-09-254-465A-1	Sequence 1, Appl
96	92.5	5.2	299	4	US-09-312-283C-189	Sequence 189, App
97	92.5	5.2	299	4	US-09-312-283C-331	Sequence 331, App
98	92.5	5.2	299	4	US-09-907-794A-119	Sequence 119, App
99	92.5	5.2	299	4	US-09-905-125A-119	Sequence 119, App
100	92.5	5.2	299	4	US-09-902-775A-119	Sequence 119, App

101	92	5.2	491	4	US-09-181-339-12	Sequence 12, Appl	174	86	4.9	985	4	US-09-877-730-10	Sequence 10, Appl
102	91	5.1	251	6	5185441-38	Patent No. 5185441	175	86	4.9	991	4	US-09-877-730-12	Sequence 12, Appl
103	90.5	5.1	521	3	US-08-996-338-20	Sequence 20, Appl	176	86	4.9	1069	4	US-09-877-730-2	Sequence 2, Appl
104	90.5	5.1	521	4	US-09-556-972-20	Sequence 20, Appl	177	86	4.9	1072	4	US-09-877-730-18	Sequence 18, Appl
105	90	5.1	156	4	US-09-370-838-210	Sequence 210, App	178	86	4.9	1150	4	US-09-877-730-8	Sequence 8, Appl
106	90	5.1	222	1	US-08-328-152A-8	Sequence 8, Appl	179	85.5	4.8	746	2	US-08-838-219B-6	Sequence 6, Appl
107	90	5.1	240	1	US-07-940-861-12	Sequence 12, Appl	180	85.5	4.8	746	3	US-09-233-336A-6	Sequence 6, Appl
108	90	5.1	240	1	US-08-459-513-12	Sequence 12, Appl	181	85.5	4.8	746	3	US-09-233-752A-6	Sequence 6, Appl
109	90	5.1	240	2	US-08-459-657-12	Sequence 12, Appl	182	85.5	4.8	746	3	US-09-402-036-6	Sequence 6, Appl
110	90	5.1	240	2	US-08-460-132-12	Sequence 12, Appl	183	85.5	4.8	746	4	US-09-904-226-6	Sequence 6, Appl
111	90	5.1	240	3	US-08-466-465-4	Sequence 4, Appl	184	85.5	4.8	789	1	US-08-471-033-29	Sequence 29, Appl
112	90	5.1	240	5	PCT-US92-02050-12	Sequence 12, Appl	185	85.5	4.8	789	1	US-08-471-033-32	Sequence 32, Appl
113	90	5.1	240	6	5185441-36	Patent No. 5185441	186	85.5	4.8	789	2	US-08-471-044-29	Sequence 29, Appl
114	90	5.1	240	6	5223394-4	Patent No. 5223394	187	85.5	4.8	789	2	US-08-471-044-32	Sequence 32, Appl
115	90	5.1	240	6	5223394-6	Patent No. 5223394	188	85.5	4.8	789	2	US-08-463-483A-29	Sequence 29, Appl
116	90	5.1	250	1	US-07-940-861-10	Sequence 10, Appl	189	85.5	4.8	789	2	US-08-463-483A-32	Sequence 32, Appl
117	90	5.1	250	1	US-08-459-512-10	Sequence 10, Appl	190	85.5	4.8	789	2	US-08-471-046A-29	Sequence 29, Appl
118	90	5.1	250	2	US-08-459-657-10	Sequence 10, Appl	191	85.5	4.8	789	2	US-08-471-046A-32	Sequence 32, Appl
119	90	5.1	250	2	US-08-460-132-10	Sequence 10, Appl	192	85.5	4.8	789	2	US-08-470-566B-29	Sequence 29, Appl
120	90	5.1	250	3	US-08-466-465-2	Sequence 2, Appl	193	85.5	4.8	789	2	US-08-470-566B-32	Sequence 32, Appl
121	90	5.1	250	5	PCT-US92-02050-10	Sequence 10, Appl	194	85.5	4.8	789	2	US-08-838-219B-2	Sequence 2, Appl
122	90	5.1	250	6	5223394-1	Patent No. 5223394	195	85.5	4.8	789	2	US-08-838-219B-4	Sequence 4, Appl
123	90	5.1	419	6	5169835-2	Patent No. 5169835	196	85.5	4.8	789	2	US-08-469-334-29	Sequence 29, Appl
124	90	5.1	541	1	US-08-604-333-2	Sequence 2, Appl	197	85.5	4.8	789	3	US-08-469-334-32	Sequence 32, Appl
125	90	5.1	541	3	US-09-110-618-2	Sequence 2, Appl	198	85.5	4.8	789	3	US-09-300-529-29	Sequence 29, Appl
126	90	5.1	541	4	US-09-173-151A-28	Sequence 28, Appl	199	85.5	4.8	789	3	US-09-300-529-32	Sequence 32, Appl
127	90	5.1	541	4	US-09-578-178-2	Sequence 2, Appl	200	85.5	4.8	789	3	US-09-233-336A-2	Sequence 2, Appl
128	90	5.1	541	4	US-09-577-806-2	Sequence 2, Appl	201	85.5	4.8	789	3	US-09-233-336A-4	Sequence 4, Appl
129	90	5.1	541	4	US-09-621-502-4	Sequence 4, Appl	202	85.5	4.8	789	3	US-09-233-752A-2	Sequence 2, Appl
130	89.5	5.1	423	4	US-09-181-339-9	Sequence 9, Appl	203	85.5	4.8	789	3	US-09-233-752A-4	Sequence 4, Appl
131	89	5.0	303	4	US-09-651-200-23	Sequence 23, Appl	204	85.5	4.8	789	3	US-09-402-036-2	Sequence 2, Appl
132	89	5.0	309	2	US-08-456-104-4	Sequence 4, Appl	205	85.5	4.8	789	3	US-09-402-036-4	Sequence 4, Appl
133	89	5.0	309	3	US-08-479-744A-23	Sequence 23, Appl	206	85.5	4.8	789	4	US-09-002-285-78	Sequence 78, Appl
134	89	5.0	309	3	US-08-280-757B-23	Sequence 23, Appl	207	85.5	4.8	789	4	US-09-002-285-80	Sequence 80, Appl
135	89	5.0	309	3	US-08-205-697A-13	Sequence 13, Appl	208	85.5	4.8	789	4	US-09-002-285-94	Sequence 94, Appl
136	89	5.0	309	3	US-08-702-525-21	Sequence 21, Appl	209	85.5	4.8	789	4	US-09-002-285-100	Sequence 100, App
137	89	5.0	309	4	US-09-651-200-22	Sequence 22, Appl	210	85.5	4.8	789	4	US-09-904-226-2	Sequence 2, Appl
138	89	5.0	309	4	US-09-667-135-33	Sequence 33, Appl	211	85.5	4.8	789	4	US-09-904-226-4	Sequence 4, Appl
139	89	5.0	309	4	US-09-425-762-23	Sequence 23, Appl	212	85.5	4.8	789	4	US-09-589-477-78	Sequence 78, Appl
140	89	5.0	309	4	US-09-837-867A-21	Sequence 21, Appl	213	85.5	4.8	789	4	US-09-589-477-80	Sequence 80, Appl
141	89	5.0	309	5	PCT-US95-02576-21	Sequence 21, Appl	214	85.5	4.8	789	4	US-09-589-477-94	Sequence 94, Appl
142	89	5.0	314	3	US-08-205-697A-13	Sequence 13, Appl	215	85.5	4.8	789	4	US-09-589-477-100	Sequence 100, App
143	89	5.0	314	3	US-08-702-525-13	Sequence 13, Appl	216	85.5	4.8	789	4	US-09-960-780-8	Sequence 8, Appl
144	89	5.0	314	4	US-09-837-867A-13	Sequence 13, Appl	217	85.5	4.8	790	3	US-09-073-898-8	Sequence 8, Appl
145	89	5.0	314	5	PCT-US95-02576-13	Sequence 13, Appl	218	85.5	4.8	790	4	US-09-307-106-2	Sequence 2, Appl
146	89	5.0	821	9	US-09-422-869-24	Sequence 24, Appl	219	85.5	4.8	790	4	US-09-850-351A-8	Sequence 8, Appl
147	88.5	5.0	611	2	US-08-752-307B-10	Sequence 10, Appl	220	85.5	4.8	2491	4	US-09-207-363-1	Sequence 1, Appl
148	88.5	5.0	611	4	US-09-707-802-10	Sequence 10, Appl	221	85	4.8	512	4	US-08-999-689A-7	Sequence 7, Appl
149	88.5	5.0	611	4	US-09-991-326-10	Sequence 10, Appl	222	85	4.8	757	3	US-08-434-000A-6	Sequence 6, Appl
150	88	5.0	699	1	US-09-651-200-19	Sequence 19, Appl	223	85	4.8	757	4	US-09-312-157-6	Sequence 6, Appl
151	88	5.0	699	2	US-08-348-006B-7	Sequence 7, Appl	224	85	4.8	821	4	US-09-622-880B-15	Sequence 15, Appl
152	88	5.0	699	2	US-08-800-823A-7	Sequence 7, Appl	225	84.5	4.8	803	3	US-08-985-950-2	Sequence 2, Appl
153	88	5.0	699	3	US-09-158-657-7	Sequence 7, Appl	226	84.5	4.8	303	4	US-09-546-049-2	Sequence 2, Appl
154	87.5	4.9	325	4	US-09-651-200-20	Sequence 20, Appl	227	84	4.7	339	4	US-09-719-243-2	Sequence 2, Appl
155	87.5	4.9	769	3	US-08-434-000A-10	Sequence 10, Appl	228	84	4.7	358	4	US-09-719-243-3	Sequence 3, Appl
156	87.5	4.9	769	4	US-09-312-157-10	Sequence 10, Appl	229	84	4.7	668	1	US-08-530-950-13	Sequence 13, Appl
157	87	4.9	490	4	US-09-336-643A-6	Sequence 6, Appl	230	84	4.7	668	3	US-09-149-879-13	Sequence 13, Appl
158	87	4.9	491	4	US-09-181-339-7	Sequence 7, Appl	231	84	4.7	668	4	US-09-057-009-13	Sequence 13, Appl
159	87	4.9	582	4	US-09-702-705-334	Sequence 334, App	232	83.5	4.7	260	4	US-09-254-465A-23	Sequence 23, Appl
160	87	4.9	582	4	US-09-736-457-334	Sequence 334, App	233	83.5	4.7	293	4	US-09-254-465A-25	Sequence 25, Appl
161	87	4.9	582	4	US-09-614-124B-334	Sequence 334, App	234	83.5	4.7	268	4	US-09-152-060-76	Sequence 76, Appl
162	87	4.9	582	4	US-09-671-325-334	Sequence 334, App	235	83.5	4.7	312	4	US-09-254-465A-9	Sequence 9, Appl
163	87	4.9	582	4	US-09-589-184-334	Sequence 334, App	236	83.5	4.7	312	4	US-09-907-794A-64	Sequence 64, Appl
164	87	4.9	583	2	US-08-432-016-2	Sequence 2, Appl	237	83.5	4.7	312	4	US-09-905-125A-64	Sequence 64, Appl
165	87	4.9	583	2	US-08-684-590-4	Sequence 2, Appl	238	83.5	4.7	312	4	US-09-902-775A-64	Sequence 64, Appl
166	86.5	4.9	790	3	US-08-960-780-2	Sequence 4, Appl	239	83.5	4.7	318	3	US-09-068-051A-32	Sequence 32, Appl
167	86.5	4.9	790	3	US-09-073-898A-4	Sequence 4, Appl	240	83.5	4.7	391	4	US-08-999-689A-8	Sequence 8, Appl
168	86.5	4.9	790	4	US-09-850-351A-4	Sequence 4, Appl	241	83.5	4.7	408	4	US-09-724-864-62	Sequence 62, Appl
169	86	4.9	302	4	US-09-877-730-14	Sequence 14, Appl	242	83.5	4.7	450	4	US-09-907-794A-320	Sequence 320, App
170	86	4.9	380	4	US-09-877-730-4	Sequence 4, Appl	243	83.5	4.7	450	4	US-09-905-125A-320	Sequence 320, App
171	86	4.9	826	4	US-09-877-730-16	Sequence 16, Appl	244	83.5	4.7	450	4	US-09-902-775A-320	Sequence 320, App
172	86	4.9	904	4	US-09-877-730-6	Sequence 6, Appl	245	83.5	4.7	789	4	US-09-002-285-96	Sequence 96, Appl
173	86	4.9	907	4	US-09-877-730-20	Sequence 20, Appl	246	83.5	4.7	789	4	US-09-589-477-96	Sequence 96, Appl

247	83.5	4.7	1501	2	US-08-447-464-3	Sequence 3, Appl	Sequence 3, Appl	320	80	4.5	338	2	US-08-414-657D-43	Sequence 43, Appl
248	83.5	4.7	1501	2	US-08-716-679-3	Sequence 3, Appl	Sequence 3, Appl	321	80	4.5	338	4	US-09-135-080-4	Sequence 4, Appl
249	83	4.7	1501	2	US-09-297-468-2	Sequence 2, Appl	Sequence 2, Appl	322	80	4.5	499	4	US-09-252-991A-23328	Sequence 23328, A
250	83	4.7	846	1	US-08-149-103-3	Sequence 3, Appl	Sequence 3, Appl	323	80	4.5	528	4	US-09-010-147B-20	Sequence 20, Appl
251	83	4.7	846	1	US-08-451-883-3	Sequence 3, Appl	Sequence 3, Appl	324	80	4.5	529	4	US-09-383-586-31	Sequence 31, Appl
252	83	4.7	873	1	US-08-393-734-2	Sequence 2, Appl	Sequence 2, Appl	325	80	4.5	607	2	US-08-752-307B-12	Sequence 12, Appl
253	83	4.7	873	3	US-08-894-489-2	Sequence 2, Appl	Sequence 2, Appl	326	80	4.5	607	4	US-09-707-802-12	Sequence 12, Appl
254	82.5	4.7	194	3	US-08-630-172-14	Sequence 14, Appl	Sequence 14, Appl	327	80	4.5	607	4	US-09-991-326-12	Sequence 12, Appl
255	82.5	4.7	194	3	US-09-375-419-14	Sequence 14, Appl	Sequence 14, Appl	328	80	4.5	1233	6	US-09-194-613-5	Sequence 5, Appl
256	82.5	4.7	238	4	US-09-149-476-485	Sequence 485, App	Sequence 485, App	329	79.5	4.5	202	6	5189147-6	Patent No. 5189147
257	82.5	4.7	486	4	US-09-134-000C-5552	Sequence 5552, Ap	Sequence 5552, Ap	330	79.5	4.5	278	4	US-09-570-367C-21	Sequence 21, Appl
258	82.5	4.7	511	4	US-09-002-285-88	Sequence 88, Appl	Sequence 88, Appl	331	79.5	4.5	278	4	US-09-915-524-21	Sequence 21, Appl
259	82.5	4.7	511	4	US-09-589-477-88	Sequence 88, Appl	Sequence 88, Appl	332	79.5	4.5	328	3	US-08-821-994-84	Sequence 84, Appl
260	82.5	4.7	789	4	US-09-002-285-82	Sequence 82, Appl	Sequence 82, Appl	333	79.5	4.5	335	4	US-09-489-039A-11298	Sequence 11298, A
261	82.5	4.7	789	4	US-09-002-285-84	Sequence 84, Appl	Sequence 84, Appl	334	79.5	4.5	374	3	US-08-821-994-68	Sequence 68, Appl
262	82.5	4.7	789	4	US-09-002-285-92	Sequence 92, Appl	Sequence 92, Appl	335	79.5	4.5	402	4	US-09-293-097-16	Sequence 16, Appl
263	82.5	4.7	789	4	US-09-589-477-82	Sequence 82, Appl	Sequence 82, Appl	336	79.5	4.5	643	1	US-09-471-570-6	Sequence 6, Appl
264	82.5	4.7	789	4	US-09-589-477-84	Sequence 84, Appl	Sequence 84, Appl	337	79.5	4.5	769	1	US-08-471-570-8	Sequence 8, Appl
265	82.5	4.7	789	4	US-09-589-477-92	Sequence 92, Appl	Sequence 92, Appl	338	79.5	4.5	859	4	US-09-788-200-7	Sequence 7, Appl
266	82.5	4.7	790	4	US-09-002-285-102	Sequence 102, App	Sequence 102, App	339	79.5	4.5	859	4	US-09-788-657-16	Sequence 16, Appl
267	82.5	4.7	790	4	US-09-589-477-102	Sequence 102, App	Sequence 102, App	340	79.5	4.5	439	1	US-08-429-742-2	Sequence 22, Appl
268	82	4.6	314	4	US-09-107-532A-4919	Sequence 4919, Ap	Sequence 4919, Ap	341	78.5	4.4	439	3	US-09-383-586-32	Sequence 32, Appl
269	82	4.6	449	3	US-09-118-319-7	Sequence 7, Appl	Sequence 7, Appl	342	78.5	4.4	831	2	US-09-047-036A-4	Sequence 4, Appl
270	82	4.6	449	3	US-09-286-691-4	Sequence 4, Appl	Sequence 4, Appl	343	78	4.4	341	1	US-08-248-628A-2	Sequence 2, Appl
271	82	4.6	449	3	US-09-687-147-4	Sequence 4, Appl	Sequence 4, Appl	344	78	4.4	345	4	US-09-214-631-5	Sequence 5, Appl
272	82	4.6	757	4	US-09-622-880B-1	Sequence 1, Appl	Sequence 1, Appl	345	78	4.4	624	2	US-08-642-406A-22	Sequence 22, Appl
273	82	4.6	874	2	US-08-456-647B-6	Sequence 6, Appl	Sequence 6, Appl	346	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
274	82	4.6	874	2	US-08-237-401A-6	Sequence 6, Appl	Sequence 6, Appl	347	78	4.4	624	4	US-09-199-534-22	Sequence 22, Appl
275	82	4.6	880	1	US-08-445-640-10	Sequence 10, Appl	Sequence 10, Appl	348	77.5	4.4	321	4	US-09-254-465A-2	Sequence 2, Appl
276	82	4.6	880	3	US-08-170-558-10	Sequence 10, Appl	Sequence 10, Appl	349	77.5	4.4	477	2	US-08-432-016-3	Sequence 3, Appl
277	82	4.6	880	3	US-08-447-314-10	Sequence 10, Appl	Sequence 10, Appl	350	77.5	4.4	477	2	US-08-684-594-3	Sequence 3, Appl
278	82	4.6	880	3	US-08-445-461-10	Sequence 10, Appl	Sequence 10, Appl	351	77.5	4.4	650	4	US-09-310-463-2	Sequence 2, Appl
279	81.5	4.6	309	4	US-09-667-135-6	Sequence 6, Appl	Sequence 6, Appl	352	77.5	4.4	650	4	US-08-842-248A-2	Sequence 2, Appl
280	81.5	4.6	309	4	US-09-910-174B-7	Sequence 7, Appl	Sequence 7, Appl	353	77.5	4.4	662	1	US-08-261-304-7	Sequence 7, Appl
281	81.5	4.6	309	4	US-09-620-461-7	Sequence 7, Appl	Sequence 7, Appl	354	77.5	4.4	735	5	PCT-US93-00031-13	Sequence 13, Appl
282	81.5	4.6	558	4	US-09-667-135-31	Sequence 31, Appl	Sequence 31, Appl	355	77.5	4.4	736	5	PCT-US93-00031-15	Sequence 15, Appl
283	81.5	4.6	846	1	US-08-149-103-4	Sequence 4, Appl	Sequence 4, Appl	356	77.5	4.4	739	4	US-08-482-073-6	Sequence 6, Appl
284	81.5	4.6	846	1	US-08-451-883-4	Sequence 4, Appl	Sequence 4, Appl	357	77.5	4.4	1312	4	US-09-554-572-26	Sequence 26, Appl
285	81	4.6	144	6	5169835-8	Patent No. 5169835	Patent No. 5169835	358	77.5	4.4	1312	4	US-09-554-572-26	Sequence 26, Appl
286	81	4.6	252	2	US-08-414-657D-56	Sequence 56, Appl	Sequence 56, Appl	359	77	4.3	278	4	US-09-570-367C-2	Sequence 2, Appl
287	81	4.6	287	2	US-08-414-657D-48	Sequence 48, Appl	Sequence 48, Appl	360	77	4.3	278	4	US-09-915-524-2	Sequence 2, Appl
288	81	4.6	304	2	US-08-414-657D-44	Sequence 44, Appl	Sequence 44, Appl	361	77	4.3	458	4	US-09-433-956A-1	Sequence 1, Appl
289	81	4.6	308	2	US-08-414-657D-46	Sequence 46, Appl	Sequence 46, Appl	362	77	4.3	523	3	US-08-948-564-8	Sequence 8, Appl
290	81	4.6	325	2	US-08-414-657D-2	Sequence 2, Appl	Sequence 2, Appl	363	77	4.3	1021	1	US-08-497-025-3	Sequence 3, Appl
291	81	4.6	325	2	US-08-414-657D-41	Sequence 41, Appl	Sequence 41, Appl	364	77	4.3	1033	4	US-09-252-991A-20611	Sequence 20611, A
292	81	4.6	325	2	US-09-135-080-2	Sequence 2, Appl	Sequence 2, Appl	365	76.5	4.3	292	4	US-09-800-729-175	Sequence 175, App
293	81	4.6	338	2	US-08-414-657D-60	Sequence 60, Appl	Sequence 60, Appl	366	76.5	4.3	364	4	US-08-896-537A-3	Sequence 3, Appl
294	81	4.6	338	4	US-09-135-080-8	Sequence 8, Appl	Sequence 8, Appl	367	76.5	4.3	364	4	US-09-667-135-28	Sequence 28, Appl
295	81	4.6	338	4	US-09-976-594-404	Sequence 404, App	Sequence 404, App	368	76.5	4.3	589	4	US-09-866-510-12	Sequence 12, Appl
296	80.5	4.5	205	4	US-09-134-001C-4766	Sequence 4766, Ap	Sequence 4766, Ap	369	76.5	4.3	1089	1	US-08-180-195-36	Sequence 36, Appl
297	80.5	4.5	346	1	US-08-213-003-2	Sequence 2, Appl	Sequence 2, Appl	370	76.5	4.3	1089	1	US-08-168-917-4	Sequence 4, Appl
298	80.5	4.5	346	1	US-08-458-077-2	Sequence 2, Appl	Sequence 2, Appl	371	76.5	4.3	1089	1	US-08-477-329-36	Sequence 36, Appl
299	80.5	4.5	346	1	US-08-460-741-2	Sequence 2, Appl	Sequence 2, Appl	372	76.5	4.3	1089	2	US-08-475-458-36	Sequence 36, Appl
300	80.5	4.5	346	1	US-08-747-240-2	Sequence 2, Appl	Sequence 2, Appl	373	76.5	4.3	1089	2	US-08-460-510-4	Sequence 4, Appl
301	80.5	4.5	346	1	US-08-299-567-6	Sequence 6, Appl	Sequence 6, Appl	374	76.5	4.3	1089	3	US-08-460-490-4	Sequence 4, Appl
302	80.5	4.5	346	1	US-09-039-642B-2	Sequence 2, Appl	Sequence 2, Appl	375	76.5	4.3	1089	3	US-08-980-400-36	Sequence 36, Appl
303	80.5	4.5	650	1	US-08-121-713D-60	Sequence 60, Appl	Sequence 60, Appl	376	76.5	4.3	1089	3	US-08-462-728-2	Sequence 2, Appl
304	80.5	4.5	650	1	US-08-835-268-60	Sequence 60, Appl	Sequence 60, Appl	377	76.5	4.3	1089	3	US-09-583-459A-36	Sequence 36, Appl
305	80.5	4.5	650	2	US-09-060-692-60	Sequence 60, Appl	Sequence 60, Appl	378	76.5	4.3	1089	3	US-09-583-210-35	Sequence 36, Appl
306	80.5	4.5	650	3	US-08-833-391-60	Sequence 60, Appl	Sequence 60, Appl	379	76.5	4.3	1089	4	US-09-583-449A-36	Sequence 36, Appl
307	80.5	4.5	650	4	US-09-060-610-60	Sequence 60, Appl	Sequence 60, Appl	380	76.5	4.3	1089	4	US-09-435-059-36	Sequence 36, Appl
308	80.5	4.5	650	5	PCT-US94-10151A-60	Sequence 60, Appl	Sequence 60, Appl	381	76.5	4.3	1089	4	US-08-461-917-2	Sequence 2, Appl
309	80.5	4.5	721	4	US-09-390-234-20	Sequence 20, Appl	Sequence 20, Appl	382	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appl
310	80.5	4.5	721	4	US-09-603-311-20	Sequence 20, Appl	Sequence 20, Appl	383	76.5	4.3	1089	4	US-08-464-436-2	Sequence 2, Appl
311	80.5	4.5	789	3	US-08-960-780-6	Sequence 6, Appl	Sequence 6, Appl	384	76.5	4.3	1089	4	US-09-769-987-2	Sequence 2, Appl
312	80.5	4.5	789	3	US-09-073-898-6	Sequence 6, Appl	Sequence 6, Appl	385	76.5	4.3	1089	4	US-09-866-510-2	Sequence 2, Appl
313	80.5	4.5	789	4	US-09-850-351A-6	Sequence 6, Appl	Sequence 6, Appl	386	76.5	4.3	1089	4	US-09-866-510-4	Sequence 4, Appl
314	80.5	4.5	828	1	US-08-261-304-2	Sequence 2, Appl	Sequence 2, Appl	387	76.5	4.3	1089	4	US-09-866-510-6	Sequence 6, Appl
315	80	4.5	252	2	US-08-414-657D-57	Sequence 57, Appl	Sequence 57, Appl	388	76.5	4.3	1089	4	US-09-866-510-8	Sequence 8, Appl
316	80	4.5	287	2	US-08-414-657D-49	Sequence 49, Appl	Sequence 49, Appl	389	76.5	4.3	1089	4	US-09-866-510-10	Sequence 10, Appl
317	80	4.5	310	2	US-08-414-657D-45	Sequence 45, Appl	Sequence 45, Appl	390	76.5	4.3	1089	5	PCT-US92-00730-4	Sequence 4, Appl
318	80	4.5	315	2	US-08-414-657D-47	Sequence 47, Appl	Sequence 47, Appl	391	76.5	4.3	1089	5	PCT-US92-00862-4	Sequence 4, Appl
319	80	4.5	338	2	US-08-414-657D-42	Sequence 42, Appl	Sequence 42, Appl	392	76.5	4.3	1328	3	US-08-781-891-76	Sequence 76, Appl

393	76.5	4.3	1328	4	US-09-618-166-76	Sequence 76, Appl	466	73	4.1	112	3	US-08-545-809A-136	Sequence 136, Appl
394	76.5	4.3	1723	4	US-09-194-612A-31	Sequence 31, Appl	467	73	4.1	389	4	US-08-724-378D-3	Sequence 3, Appl
395	76.5	4.3	1745	4	US-09-800-729-89	Sequence 89, Appl	468	73	4.1	459	1	US-08-157-101A-7	Sequence 7, Appl
396	76	4.3	277	4	US-03-543-681A-4527	Sequence 4527, Ap	469	73	4.1	501	2	US-08-408-095-31	Sequence 31, Appl
397	76	4.3	378	1	US-08-225-477B-9	Sequence 9, Appl	470	73	4.1	504	4	US-08-868-373-6	Sequence 6, Appl
398	76	4.3	378	5	PCT-US95-04353-9	Sequence 9, Appl	471	73	4.1	548	4	US-09-398-335A-12	Sequence 12, Appl
399	76	4.3	390	3	US-08-961-564A-2	Sequence 2, Appl	472	73	4.1	548	4	US-09-887-586A-12	Sequence 12, Appl
400	76	4.3	390	4	US-09-050-861B-2	Sequence 2, Appl	473	73	4.1	548	4	US-09-895-752-12	Sequence 12, Appl
401	76	4.3	463	3	US-09-082-310-1	Sequence 1, Appl	474	73	4.1	548	4	US-09-903-012B-12	Sequence 12, Appl
402	76	4.3	463	4	US-09-575-205-1	Sequence 1, Appl	475	73	4.1	548	4	US-09-900-797-12	Sequence 12, Appl
403	76	4.3	463	4	US-09-976-594-721	Sequence 721, App	476	73	4.1	651	3	US-08-985-950-22	Sequence 22, Appl
404	76	4.3	599	1	US-08-442-542-18	Sequence 18, Appl	477	73	4.1	651	4	US-09-546-049-22	Sequence 22, Appl
405	76	4.3	599	3	US-08-765-469-18	Sequence 18, Appl	478	72.5	4.1	293	6	518947-3	Patent No. 5189147
406	75.5	4.3	648	2	US-08-817-436A-2	Sequence 2, Appl	479	72.5	4.1	331	1	US-08-364-081-3	Sequence 3, Appl
407	75	4.2	303	4	US-09-509-347-7	Sequence 7, Appl	480	72.5	4.1	331	1	US-08-630-552-3	Sequence 3, Appl
408	75	4.2	512	3	US-08-356-818A-2	Sequence 2, Appl	481	72.5	4.1	331	5	PCT-US95-16558-3	Sequence 3, Appl
409	75	4.2	527	4	US-09-510-174B-10	Sequence 10, Appl	482	72.5	4.1	347	4	US-09-667-135-4	Sequence 4, Appl
410	75	4.2	527	4	US-09-620-461-10	Sequence 10, Appl	483	72.5	4.1	354	6	5169835-4	Patent No. 5169835
411	75	4.2	641	3	US-09-422-869-26	Sequence 26, Appl	484	72.5	4.1	374	3	US-08-821-994-70	Sequence 70, Appl
412	75	4.2	855	4	US-09-328-352-6216	Sequence 6216, Ap	485	72.5	4.1	390	2	US-08-979-424-1	Sequence 1, Appl
413	75	4.2	1729	4	US-09-696-115B-2	Sequence 2, Appl	486	72.5	4.1	390	4	US-09-907-794A-39	Sequence 39, Appl
414	75	4.2	2137	4	US-09-134-001C-4463	Sequence 4463, Ap	487	72.5	4.1	390	4	US-09-905-125A-39	Sequence 39, Appl
415	74.5	4.2	218	3	US-09-068-655-7	Sequence 7, Appl	488	72.5	4.1	390	4	US-09-902-775A-39	Sequence 39, Appl
416	74.5	4.2	230	6	5169835-13	Patent No. 5169835	489	72.5	4.1	424	6	5169835-6	Patent No. 5169835
417	74.5	4.2	338	4	US-09-688-188B-152	Sequence 152, App	490	72.5	4.1	489	4	US-09-134-001C-4902	Sequence 4902, Ap
418	74.5	4.2	338	4	US-09-291-417D-152	Sequence 152, App	491	72.5	4.1	521	2	US-08-504-048-9	Sequence 9, Appl
419	74.5	4.2	373	4	US-09-688-188B-97	Sequence 97, Appl	492	72.5	4.1	526	1	US-08-471-570-4	Sequence 4, Appl
420	74.5	4.2	373	4	US-09-291-417D-97	Sequence 97, Appl	493	72.5	4.1	560	4	US-09-071-035-220	Sequence 220, App
421	74.5	4.2	374	3	US-08-821-994-67	Sequence 67, Appl	494	72.5	4.1	605	2	US-08-752-307B-8	Sequence 8, Appl
422	74.5	4.2	374	3	US-08-821-994-69	Sequence 69, Appl	495	72.5	4.1	605	4	US-09-707-807B-8	Sequence 8, Appl
423	74.5	4.2	463	2	US-08-853-659A-52	Sequence 52, Appl	496	72.5	4.1	605	4	US-09-931-326-8	Sequence 8, Appl
424	74.5	4.2	789	4	US-09-002-285-98	Sequence 98, Appl	497	72.5	4.1	627	4	US-09-071-035-218	Sequence 218, App
425	74.5	4.2	789	4	US-09-589-477-98	Sequence 98, Appl	498	72.5	4.1	652	1	US-08-471-570-10	Sequence 10, Appl
426	74.5	4.2	1018	1	US-08-452-052-2	Sequence 2, Appl	499	72.5	4.1	659	4	US-09-134-000C-6124	Sequence 6124, Ap
427	74.5	4.2	1148	2	US-08-313-185-58	Sequence 58, Appl	500	72.5	4.1	759	4	US-09-002-285-86	Sequence 86, Appl
428	74.5	4.2	1148	2	US-09-082-614A-58	Sequence 58, Appl	501	72.5	4.1	759	4	US-09-589-477-86	Sequence 86, Appl
429	74.5	4.2	1788	2	US-08-962-284-2	Sequence 2, Appl	502	72.5	4.1	768	4	US-09-489-039A-12897	Sequence 12897, A
430	74.5	4.2	1911	1	US-08-348-006B-5	Sequence 5, Appl	503	72.5	4.1	790	4	US-09-543-681A-5459	Sequence 5459, Ap
431	74.5	4.2	1911	2	US-08-800-825A-5	Sequence 5, Appl	504	72.5	4.1	913	4	US-09-140-378A-2	Sequence 2, Appl
432	74.5	4.2	1911	3	US-09-158-657-5	Sequence 5, Appl	505	72.5	4.1	919	1	US-08-336-343A-2	Sequence 2, Appl
433	74.5	4.2	1911	5	PCT-US94-10166-5	Sequence 5, Appl	506	72.5	4.1	1434	2	US-08-540-406-10	Sequence 10, Appl
434	74.5	4.2	4654	3	US-08-476-515A-84	Sequence 84, Appl	507	72.5	4.1	1434	3	US-08-656-055-10	Sequence 10, Appl
435	74.5	4.2	4655	3	US-08-652-877-84	Sequence 84, Appl	508	72.5	4.1	1434	3	US-08-954-668-10	Sequence 10, Appl
436	74.5	4.2	4655	3	US-08-652-877-86	Sequence 86, Appl	509	72.5	4.1	1434	3	US-08-918-658-10	Sequence 10, Appl
437	74.5	4.2	4655	3	US-08-652-877-88	Sequence 88, Appl	510	72.5	4.1	1434	4	US-09-724-631-10	Sequence 10, Appl
438	74.5	4.2	4655	3	US-08-652-877-90	Sequence 90, Appl	511	72.5	4.1	1434	4	US-08-954-701A-10	Sequence 10, Appl
439	74	4.2	343	4	US-09-454-034-8	Sequence 8, Appl	512	72.5	4.1	1434	5	PCT-US95-13233-10	Sequence 10, Appl
440	74	4.2	387	4	US-09-175-928-2	Sequence 2, Appl	513	72	4.1	311	4	US-09-252-991A-28792	Sequence 28792, A
441	74	4.2	451	4	US-09-107-532A-6652	Sequence 6652, Ap	514	72	4.1	328	4	US-09-489-039A-13216	Sequence 13216, A
442	74	4.2	543	4	US-09-042-709A-18	Sequence 18, Appl	515	72	4.1	348	2	US-09-031-485-28	Sequence 28, Appl
443	74	4.2	548	1	US-08-247-902A-2	Sequence 2, Appl	516	72	4.1	348	2	US-08-847-429A-28	Sequence 28, Appl
444	74	4.2	548	5	PCT-US93-10541-2	Sequence 2, Appl	517	72	4.1	348	3	US-09-065-474-28	Sequence 28, Appl
445	74	4.2	862	4	US-08-556-422A-2	Sequence 2, Appl	518	72	4.1	348	4	US-09-557-034-28	Sequence 28, Appl
446	74	4.2	1027	1	US-09-162-021B-2	Sequence 2, Appl	519	72	4.1	379	4	US-09-186-276B-46	Sequence 46, Appl
447	74	4.2	1333	1	US-08-447-411-76	Sequence 76, Appl	520	72	4.1	379	4	US-08-842-445-46	Sequence 46, Appl
448	74	4.2	1333	2	US-08-662-227-34	Sequence 34, Appl	521	72	4.1	456	1	US-09-186-188B-46	Sequence 46, Appl
449	74	4.2	1333	4	US-09-017-947-34	Sequence 34, Appl	522	72	4.1	456	5	PCT-US96-06035-6	Sequence 6, Appl
450	74	4.2	1333	4	US-09-925-442-34	Sequence 34, Appl	523	72	4.1	456	5	US-08-435-933-6	Sequence 6, Appl
451	73.5	4.1	217	4	US-09-134-001C-5638	Sequence 5638, Ap	524	72	4.1	497	4	US-08-709-731A-29	Sequence 29, Appl
452	73.5	4.1	238	4	US-08-978-289-10	Sequence 10, Appl	525	72	4.1	517	4	US-09-723-368-4	Sequence 4, Appl
453	73.5	4.1	321	4	US-09-171-461-22	Sequence 22, Appl	526	72	4.1	548	4	US-09-398-395A-2	Sequence 2, Appl
454	73.5	4.1	344	4	US-09-700-397-3	Sequence 3, Appl	527	72	4.1	548	4	US-09-887-586A-2	Sequence 2, Appl
455	73.5	4.1	513	4	US-09-910-174B-18	Sequence 18, Appl	528	72	4.1	548	4	US-09-895-752-2	Sequence 2, Appl
456	73.5	4.1	513	4	US-09-620-461-18	Sequence 18, Appl	529	72	4.1	548	4	US-09-903-012B-2	Sequence 2, Appl
457	73.5	4.1	699	4	US-09-134-001C-4054	Sequence 4054, Ap	530	72	4.1	548	4	US-09-900-797-2	Sequence 2, Appl
458	73.5	4.1	716	3	US-09-171-945-125	Sequence 125, App	531	72	4.1	548	2	US-08-525-864A-2	Sequence 2, Appl
459	73.5	4.1	913	1	US-08-445-640-4	Sequence 4, Appl	532	72	4.1	754	2	US-09-319-588C-18	Sequence 18, Appl
460	73.5	4.1	913	3	US-08-170-558-4	Sequence 4, Appl	533	72	4.1	852	4	US-09-540-245A-17	Sequence 17, Appl
461	73.5	4.1	913	3	US-08-447-314-4	Sequence 4, Appl	534	72	4.1	1297	3	US-09-489-039A-13216	Sequence 13216, A
462	73.5	4.1	913	3	US-08-445-461-4	Sequence 4, Appl	535	72	4.1	1456	1	US-08-803-973-2	Sequence 2, Appl
463	73.5	4.1	1000	4	US-08-193-562D-30	Sequence 30, Appl	536	72	4.1	1456	1	US-08-803-972-2	Sequence 2, Appl
464	73.5	4.1	4544	1	US-08-469-486-52	Sequence 52, Appl	537	72	4.1	1745	2	US-09-031-485-33	Sequence 33, Appl
465	73.5	4.1	4544	2	US-08-469-658-52	Sequence 52, Appl	538	72	4.1	1745	3	US-09-065-474-33	Sequence 33, Appl

539	72	4.1	1745	4	US-09-557-034-33	Sequence 33, Appl	612	71	4.0	1338	4	US-09-119-014D-6	Sequence 6, Appli
540	71.5	4.0	206	3	US-08-821-994-77	Sequence 77, Appl	613	71	4.0	1362	2	US-08-874-678-33	Sequence 33, Appl
541	71.5	4.0	248	6	5169835-15	Patent No. 5169835	614	71	4.0	1362	2	US-08-643-839-33	Sequence 33, Appl
542	71.5	4.0	327	3	US-09-173-581-5	Sequence 5, Appli	615	71	4.0	1362	4	US-09-348-886-33	Sequence 33, Appl
543	71.5	4.0	327	3	US-09-420-915-5	Sequence 5, Appli	616	71	4.0	1481	2	US-08-616-844-40	Sequence 40, Appl
544	71.5	4.0	384	4	US-09-552-122-2	Sequence 2, Appli	617	71	4.0	1481	2	US-08-593-654-40	Sequence 40, Appl
545	71.5	4.0	403	4	US-09-638-643-5	Sequence 5, Appli	618	71	4.0	1481	3	US-08-944-869A-40	Sequence 40, Appl
546	71.5	4.0	462	4	US-09-166-350-18	Sequence 18, Appl	619	71	4.0	1481	3	US-08-944-423A-40	Sequence 40, Appl
547	71.5	4.0	523	4	US-09-910-174B-11	Sequence 11, Appl	620	71	4.0	1481	3	US-08-944-496-40	Sequence 40, Appl
548	71.5	4.0	523	4	US-09-620-461-11	Sequence 11, Appl	621	70.5	4.0	183	4	US-09-621-976-3942	Sequence 3942, Ap
549	71.5	4.0	608	4	US-09-095-385-4	Sequence 4, Appli	622	70.5	4.0	338	3	US-08-922-957-1	Sequence 1, Appli
550	71.5	4.0	746	3	US-08-434-000A-4	Sequence 4, Appli	623	70.5	4.0	338	3	US-08-922-957-3	Sequence 3, Appli
551	71.5	4.0	746	4	US-09-312-157-4	Sequence 4, Appli	624	70.5	4.0	343	4	US-09-134-000C-6363	Sequence 6363, Ap
552	71.5	4.0	919	2	US-08-788-674-4	Sequence 4, Appli	625	70.5	4.0	466	3	US-09-134-001C-3526	Sequence 3526, Ap
553	71.5	4.0	2468	4	US-09-976-594-726	Sequence 726, App	626	70.5	4.0	467	3	US-08-821-994-83	Sequence 83, Appl
554	71	4.0	107	1	US-08-425-336-125	Sequence 125, App	627	70.5	4.0	491	4	US-09-134-001C-4727	Sequence 4727, Ap
555	71	4.0	107	1	US-08-488-113B-125	Sequence 125, App	628	70.5	4.0	502	4	US-09-489-039A-8035	Sequence 8035, Ap
556	71	4.0	107	1	US-08-477-484B-125	Sequence 125, App	629	70.5	4.0	533	1	US-07-820-011A-2	Sequence 2, Appli
557	71	4.0	107	1	US-08-107-669D-65	Sequence 65, Appl	630	70.5	4.0	533	4	US-09-470-881-3	Sequence 3, Appli
558	71	4.0	107	1	US-08-472-788A-87	Sequence 87, Appl	631	70.5	4.0	533	5	PCT-US93-00445-2	Sequence 2, Appli
559	71	4.0	107	2	US-08-477-531B-65	Sequence 65, Appl	632	70.5	4.0	579	4	US-09-173-151A-2	Sequence 2, Appli
560	71	4.0	107	2	US-08-646-360-125	Sequence 125, App	633	70.5	4.0	610	4	US-09-976-594-947	Sequence 947, App
561	71	4.0	233	4	US-09-198-452A-244	Sequence 244, App	634	70.5	4.0	617	3	US-09-188-930-303	Sequence 303, App
562	71	4.0	236	3	US-09-049-672A-7	Sequence 7, Appli	635	70.5	4.0	617	4	US-09-312-283C-303	Sequence 303, App
563	71	4.0	107	3	US-08-839-765-125	Sequence 125, App	636	70.5	4.0	668	1	US-08-232-538-13	Sequence 13, Appl
564	71	4.0	107	3	US-09-136-389-125	Sequence 125, App	637	70.5	4.0	668	2	US-08-786-164-13	Sequence 13, Appl
565	71	4.0	107	4	US-09-610-838-125	Sequence 125, App	638	70.5	4.0	686	4	US-09-173-151A-4	Sequence 4, Appli
566	71	4.0	233	4	US-08-646-360-147	Sequence 147, App	639	70.5	4.0	764	4	US-09-142-956B-14	Sequence 14, Appl
567	71	4.0	236	3	US-09-049-672A-7	Sequence 7, Appli	640	70.5	4.0	767	2	US-08-874-678-2	Sequence 2, Appli
568	71	4.0	240	1	US-08-488-113B-147	Sequence 147, App	641	70.5	4.0	767	3	US-08-643-839-2	Sequence 2, Appli
569	71	4.0	240	1	US-08-488-113B-148	Sequence 148, App	642	70.5	4.0	767	4	US-09-348-886-2	Sequence 2, Appli
570	71	4.0	240	1	US-08-477-484B-147	Sequence 147, App	643	70.5	4.0	788	1	US-08-232-538-15	Sequence 15, Appl
571	71	4.0	240	1	US-08-477-484B-148	Sequence 148, App	644	70.5	4.0	788	2	US-08-786-164-15	Sequence 15, Appl
572	71	4.0	240	2	US-08-646-360-147	Sequence 147, App	645	70.5	4.0	940	4	US-09-198-452A-500	Sequence 500, App
573	71	4.0	240	2	US-08-646-360-148	Sequence 148, App	646	70.5	4.0	983	4	US-09-412-554A-2	Sequence 2, Appli
574	71	4.0	240	3	US-08-839-765-147	Sequence 147, App	647	70.5	4.0	1088	1	US-08-483-588-6	Sequence 6, Appli
575	71	4.0	240	3	US-08-839-765-148	Sequence 148, App	648	70.5	4.0	1088	1	US-08-484-565-6	Sequence 6, Appli
576	71	4.0	240	3	US-09-136-389-147	Sequence 147, App	649	70.5	4.0	1088	2	US-08-480-751-6	Sequence 6, Appli
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584	71	4.0	615	4	US-09-297-937C-9	Sequence 9, Appli	657	70.5	4.0	1356	4	US-09-240-274-146	Sequence 146, App
585	71	4.0	647	3	US-08-753-007A-32	Sequence 32, Appl	658	70	4.0	126	3	US-08-821-994-43	Sequence 43, Appl
586	71	4.0	647	3	US-09-398-496-32	Sequence 32, Appl	659	70	4.0	167	3	US-09-252-991A-32836	Sequence 32836, A
587	71	4.0	661	1	US-08-232-538-12	Sequence 12, Appl	660	70	4.0	313	4	US-09-036-987A-14	Sequence 14, Appl
588	71	4.0	661	2	US-08-786-164-12	Sequence 6, Appli	661	70	4.0	320	3	US-09-370-700-14	Sequence 14, Appl
589	71	4.0	687	1	US-08-232-538-6	Sequence 6, Appli	662	70	4.0	320	3	US-09-603-207-14	Sequence 14, Appl
590	71	4.0	687	2	US-08-786-164-6	Sequence 6, Appli	663	70	4.0	320	4	US-08-442-043A-17	Sequence 17, Appl
591	71	4.0	687	4	US-09-427-353-2	Sequence 2, Appli	664	70	4.0	338	1	US-08-441-893A-17	Sequence 17, Appl
592	71	4.0	731	4	US-09-107-532A-6999	Sequence 6999, Ap	665	70	4.0	338	4	US-08-459-512-43	Sequence 43, Appl
593	71	4.0	758	2	US-08-874-678-1	Sequence 1, Appli	666	70	4.0	347	1	US-07-940-861-43	Sequence 43, Appl
594	71	4.0	758	3	US-08-643-839-1	Sequence 1, Appli	667	70	4.0	347	1	US-08-459-512-43	Sequence 43, Appl
595	71	4.0	758	3	US-09-051-363-24	Sequence 24, Appl	668	70	4.0	347	2	US-08-459-657-43	Sequence 43, Appl
596	71	4.0	758	4	US-09-348-886-1	Sequence 1, Appli	669	70	4.0	347	2	US-08-460-132-43	Sequence 43, Appl
597	71	4.0	780	1	US-08-232-538-14	Sequence 14, Appl	670	70	4.0	347	3	US-08-466-465-8	Sequence 8, Appli
598	71	4.0	780	2	US-08-786-164-14	Sequence 14, Appl	671	70	4.0	347	5	PCT-US92-02050-43	Sequence 43, Appl
599	71	4.0	821	2	US-08-451-822A-13	Sequence 13, Appl	672	70	4.0	412	4	US-09-543-681A-6782	Sequence 6782, Ap
600	71	4.0	821	4	US-08-323-430-13	Sequence 13, Appl	673	70	4.0	469	3	US-08-753-007A-8	Sequence 8, Appli
601	71	4.0	906	4	US-09-651-656-13	Sequence 13, Appl	674	70	4.0	469	3	US-09-398-496-8	Sequence 8, Appli
602	71	4.0	930	4	US-09-650-855-13	Sequence 13, Appl	675	70	4.0	490	4	US-09-489-039A-9610	Sequence 9610, Ap
603	71	4.0	930	4	US-09-134-001C-5314	Sequence 5314, Ap	676	70	4.0	548	4	US-09-398-395A-4	Sequence 4, Appli
604	71	4.0	930	4	US-09-386-962C-10	Sequence 10, Appl	677	70	4.0	548	4	US-09-398-395A-6	Sequence 6, Appli
605	71	4.0	975	4	US-08-695-481-4	Sequence 4, Appli	678	70	4.0	548	4	US-09-398-395A-8	Sequence 8, Appli
606	71	4.0	1018	1	US-08-408-093-6	Sequence 6, Appli	679	70	4.0	548	4	US-09-398-395A-10	Sequence 10, Appl
607	71	4.0	1018	1	US-08-408-420A-6	Sequence 6, Appli	680	70	4.0	548	4	US-09-887-586A-4	Sequence 4, Appli
608	71	4.0	1018	3	US-08-714-901-6	Sequence 6, Appli	681	70	4.0	548	4	US-09-887-586A-6	Sequence 6, Appli
609	71	4.0	1018	3	US-08-040-741-6	Sequence 6, Appli	682	70	4.0	548	4	US-09-887-586A-8	Sequence 8, Appli
610	71	4.0	1276	4	US-09-297-937C-13	Sequence 13, Appl	683	70	4.0	548	4	US-09-887-586A-10	Sequence 10, Appl
611	71	4.0	1338	3	US-08-750-141A-3	Sequence 3, Appli	684	70	4.0	548	4	US-09-895-752-4	Sequence 4, Appli

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05

EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
Query Match 20.5%; Score 362.5; DB 4; Length 329;
Best Local Similarity 31.5%; Pred. No. 1.6e-30;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;
QY 14 LWQL-----TGSAAAGPVKELV---GSVGAVTFPLK-SKVQVDSIVVMTNTPLVLTQ 64
DB 6 LWILLCLQWPEAAAGKSEIFTVNGILGESVTFPNVQEPQVKIATSKTSVAYVTP 65
QY 65 PEGGT---IIVTQNRNRERVDPPGGYSLKSLKKNDSGIYVYGIYSSLOQPSTQEV 121
DB 66 GDSFAPVTVTHRYRIHALGPNVNLVSLDMEDAGDYKADINTQADPYTTTKRYN 125
QY 122 LHVYEHLSKPKVTMGLQSNKNGTCVNTLTCNHEGSEEDVIYTKALGQANSHNGSILP 181
DB 126 LQIYRRLGPKKITQSLMASVNSTCNVTLTCSVEKEKNVTYNWSPG-----EGNV 179
QY 182 ISRWGESDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDS-----SMVLLC 235
DB 180 IFQTPEDQELTYTCTAQNPNVNN-SDSISARQLCADIAMGFRHTHTGLLSVLAMF 238
QY 236 LLLSLFVLGLFLWFLKRRERQEEYIEBKRVDCRETNPICPHSGENTYDTIPTHTN 295
DB 239 ILSSVFLFLRF-----KRRQDAASKKTIYTIMASRNTQP--AESRIYDEILQSK 290
QY 296 KEDPANTYVSTVEIPKQENPHSLTMDPTPLPAYENVI 335
DB 291 KEEPVNTYVSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 2

US-08-348-792-10
Sequence 10, Application US/08348792
Patent No. 5576423
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS, PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,792
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
.TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-792-10

Query Match 10.5%; Score 186; DB 1; Length 343;
Best Local Similarity 24.3%; Pred. No. 2.1e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;
QY 8 LTIYILWLTGSAASG---PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVMDCPV--ILQKLGQDTWLPITNEHQINKSVNKSRIIV-TMA 68
QY 57 TTPLVITIQPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
DB 69 TSP-----GSKSNKKIVSFDLSKSGYPDHLDDGYHFQSKNLSLKILGNRRS 115
QY 100 SGIYVGIYSS-SLQQPSTQEVYLVHYEHLSP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGYLVSVVENSVSQFCQKQ---LKLIEQVSPPEIKVLNKTQENENGTCSLLLACTVKG 172
QY 157 EEDVIYTWK-----ALGOANESHGSIPLISRWGESDMTFICVARNPV---SRNFSSP 208
DB 173 DH-VTYSNDEAGTHLLSRNRSH---LLHITLSNQHQDSIYNCTASNVPVSSISRTFN-- 226
QY 209 ILARKLCEGAADDPDSSMVLCLLLVPLLSLFLGLFLWFLKRRERQEEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVIFILVFTAILMMKROGKSNHCQPPVEEKS 285
QY 266 DICRETPNICPHSGENTYDTTIPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAQVQKSGQP--EKKLHD-----ALTDQDPCTTIYVAATEPAPESVQEPNPTTVA 336
QY 319 LITMPTD 325
DB 337 SVTLPS 343

RESULT 3

US-08-462-738-10
Sequence 10, Application US/08462738
Patent No. 597303
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.738
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GB
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-738-10

Query Match 10.5%; Score 186; DB 2; Length 343;
Best Local Similarity 24.3%; Pred. No. 2.1e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;
QY 8 LTIYILWLTGSAASG---PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVMDCPV--ILQKLGQDTWLPITNEHQINKSVNKSRIIV-TMA 68
QY 57 TTPLVITIQPEGGTIIVTQNRNRVDF-----PD---GGY-----SLKSLKLNKD 99
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QY 100 SGIYVGIYSS-SLQQPSTQEVYLVHYEHLSP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGYLVSVVENSVSQFCQKQ---LKLIEQVSPPEIKVLNKTQENENGTCSLLLACTVKG 172
QY 157 EEDVIYTWK-----ALGOANESHGSIPLISRWGESDMTFICVARNPV---SRNFSSP 208
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QY 209 ILARKLCEGAADDPDSSMVLCLLLVPLLSLFLGLFLWFLKRRERQEEYIE---EKRRV 265
DB 227 -LSSQACKQESSSESPWQYTLVPLGVVIFILVFTAILMMKROGKSNHCQPPVEEKS 285
QY 266 DICRETPNICPHSGENTYDTTIPHTNRTILKEDPANTVY--STVEIPKQENP-----HS 318
DB 286 TIYAQVQKSGQP--EKKLHD-----ALTDQDPCTTIYVAATEPAPESVQEPNPTTVA 336
QY 319 LITMPTD 325
DB 337 SVTLPS 343

RESULT 4

US-09-199-955-10
Sequence 10, Application US/09199955
Patent No. 6372899
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473

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; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX04366C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-199-955-10

Query Match 10.5%; Score 186; DB 4; Length 343;
Best Local Similarity 24.3%; Pred. No. 2,1e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

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QY 57 TTPLVTIQEGGTIIVTQNRNRVDF-----PD---GGY-----SLKLSLKKND 99
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DB 116 EGWYLVSVVENSVQOFCQK---LKYEQVSPPEIKVLNKTQENENGTCSSLLACTVKGK 172

QY 157 BEDVLYTWK-----ALGOANESHNGSILPISWRGESDMTFICVARNPV---SRNFSSP 208
DB 173 DH-VTYSWDEAGTHLLSRANSH---LLHITLSNQHQDSIYNCTASNVPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPDSSMVLCLLAVPLLLSLFVLGLFWLFLKRRERQEYIE---EKRRV 265
DB 227 -LSSQACKQESSESPPMQYTLVPLGVVILFVFTAIIMMKROGKSNHCOPPVEEKSL 285

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DB 337 SVTLPEP 343

RESULT 5
US-08-880-875-10
; Sequence 10, Application US/08880875
; Patent No. 6399065
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,777
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/348,792
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX04366K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-880-875-10

Query Match 10.5%; Score 186; DB 4; Length 343;
Best Local Similarity 24.3%; Pred. No. 2,1e-11;
Matches 89; Conservative 64; Mismatches 130; Indels 84; Gaps 21;

QY 8 LTLIYLWLTGSAAG-----PVKELVSGVGAVTFPL-----KSKVKQVDSIVWTFN 56
DB 12 LLFLSLAFELSYGTGGVMDCPV--ILQKLGQDTWPLTNEHQINKSVNKSVRILV-TMA 68

QY 57 TTPLVTIQEGGTIIVTQNRNRVDF-----PD---GGY-----SLKLSLKKND 99
DB 69 TSP-----GSKSNKKIVSFDLSKSGYPDHLEDGYHFOSKNLSLKILGNRRS 115

QY 100 SGIVYVGIYSS-SLOQPSTQEVVLHVYHLSKP--KVTMGLQSNKNGTCVTNLTCCMEHG 156
DB 116 EGWYLVSVVENSVQOFCQK---LKYEQVSPPEIKVLNKTQENENGTCSSLLACTVKGK 172

QY 157 BEDVLYTWK-----ALGOANESHNGSILPISWRGESDMTFICVARNPV---SRNFSSP 208
DB 173 DH-VTYSWDEAGTHLLSRANSH---LLHITLSNQHQDSIYNCTASNVPVSSISRTFN-- 226

QY 209 ILARKLCEGAADDPDSSMVLCLLAVPLLLSLFVLGLFWLFLKRRERQEYIE---EKRRV 265
DB 227 -LSSQACKQESSESPPMQYTLVPLGVVILFVFTAIIMMKROGKSNHCOPPVEEKSL 285

QY 266 DICRETPNICPSGENTYDTPHTNRTILKEDPANTVY--STVPIPKKMNPN-----HS 318
DB 286 TIYAQVQKSGPQ--EKKLHD-----ALTDQDPCTTIYVAATEPAPESVQEPNPTTYVA 336

QY 319 LLTMDPT 325
DB 337 SVTLPEP 343

RESULT 6
US-08-348-792-2
; Sequence 2, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio
; APPLICANT: Chang, Chia-Chun J.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: de Vries, Jan E.
; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
; TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute

```

STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/348,792
 APPLICATION NUMBER: US/08/348,792
 FILING DATE: 02-DEC-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0436
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 335 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-348-792-2

Query Match 10.3%; Score 182.5; DB 1; Length 335;
 Best Local Similarity 22.5%; Pred. No. 4.8e-11;
 Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYLW-QLTGSAAAGP-----VKELVGVGGAVTFPL-----KSKVKQVDSIVWT 54
 DB 7 LSLTFVLFLSLAFGASGTGGRMMNCPIRLQGLSKVLLPLTYERINKSMKSIHIVTM 66
 QY 55 FNT-----TPLVTIQP-EGGTIIIVTQNNRERVDPPDGGYSLKSLKKNDSGIYVGI 107
 DB 67 AKSLNSVENKIVSLDPEAG-----PPRYLGDYKFKYLENLTLGIRSKDEGWYMTL 122
 QY 108 YSS-SLQOPSTQEVYLVHVEHLSKPKVTMGLQSNKNGTCVNTLTCMEHGEEDVIYTW-- 164
 DB 123 EKNSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGCTTLILGCTVEKGDH-VAYSWE 178
 QY 165 KALGOAANESHGSLIPISWRGSDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
 DB 179 KAGTHPLNPANSHLSLTGLGPHADNIVICTVSPINNSQTFSP-----WPGCRDTP 232
 QY 223 DSSM-----VLLCLLLVPLLSLFLVLGLFLWFLKREOREEYIE---EKKRVDIC 268
 DB 233 SETKPWAVYAGLLGVIMILMVILQ-----LRRRGKTHYQTTVEKKSLLTY 281
 QY 269 RETPNICPHSGENTYDTIPHTNRTILKEDPANTVY--STVEIPKKNPHSL-----LT 321
 DB 282 AQVQKPGP---LQKLDSPF-----AQDPCTTIYVAATEPVPESVOETNSITVYASVT 331
 QY 322 MPDT 325
 DB 332 LPES 335

RESULT 7

US-08-462-738-2
 ; Sequence 2, Application US/08462738
 ; Patent No. 5977303
 ; GENERAL INFORMATION:
 ; APPLICANT: Aversa, Gregorio
 ; APPLICANT: Chang, Chia-Chun J.
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: de Vries, Jan B.
 ; TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
 ; SURFACE ANTIGENS; PROTEINS AND ANTIBODIES

NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/08/462,738
 APPLICATION NUMBER: US/08/462,738
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,792
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0436GB
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 335 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-462-738-2

Query Match 10.3%; Score 182.5; DB 2; Length 335;
 Best Local Similarity 22.5%; Pred. No. 4.8e-11;
 Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;

QY 8 LTLIYLW-QLTGSAAAGP-----VKELVGVGGAVTFPL-----KSKVKQVDSIVWT 54
 DB 7 LSLTFVLFLSLAFGASGTGGRMMNCPIRLQGLSKVLLPLTYERINKSMKSIHIVTM 66
 QY 55 FNT-----TPLVTIQP-EGGTIIIVTQNNRERVDPPDGGYSLKSLKKNDSGIYVGI 107
 DB 67 AKSLNSVENKIVSLDPEAG-----PPRYLGDYKFKYLENLTLGIRSKDEGWYMTL 122
 QY 108 YSS-SLQOPSTQEVYLVHVEHLSKPKVTMGLQSNKNGTCVNTLTCMEHGEEDVIYTW-- 164
 DB 123 EKNSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGCTTLILGCTVEKGDH-VAYSWE 178
 QY 165 KALGOAANESHGSLIPISWRGSDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
 DB 179 KAGTHPLNPANSHLSLTGLGPHADNIVICTVSPINNSQTFSP-----WPGCRDTP 232
 QY 223 DSSM-----VLLCLLLVPLLSLFLVLGLFLWFLKREOREEYIE---EKKRVDIC 268
 DB 233 SETKPWAVYAGLLGVIMILMVILQ-----LRRRGKTHYQTTVEKKSLLTY 281
 QY 269 RETPNICPHSGENTYDTIPHTNRTILKEDPANTVY--STVEIPKKNPHSL-----LT 321
 DB 282 AQVQKPGP---LQKLDSPF-----AQDPCTTIYVAATEPVPESVOETNSITVYASVT 331
 QY 322 MPDT 325
 DB 332 LPES 335

RESULT 8

US-09-199-955-2
 ; Sequence 2, Application US/09199955
 ; Patent No. 6372899
 ; GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS: PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,955
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,473
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436GC
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-199-955-2

Query Match 10.3%; Score 182.5; DB 4; Length 335;
Best Local Similarity 22.5%; Pred. No. 4.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;
QY 8 LTIYILM-QLTGSASGP-----VKELVSGVGAVTPPL-----KSKVKQVDSIVWT 54
DB 7 LSLTFVLFLAFGASGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIIHVMT 66
QY 55 FNT-----TPLVITQP-EGGTIIVTQNRNRVDFPDGGYSILKSLKKNDSGIYVGI 107
DB 67 AKLSLENVENKIVSLDPSEAG-----PPRYLGRYKYLENLTLGIRSRKDEGWYLMTL 122
QY 108 YSS-SLQQPSTQBYLVHVTYHLKSKPTMTGLOSNGKTCVTNLTCCMEHGEDVIYTW-- 164
DB 123 EKNVSQVRCFLQ---LRLYEQVSTPEIKVLNKTQENGCTLLIGCTVEKGDH-VAYSNSE 178
QY 165 KALQQAANSHNGSILPISWRNGESDMTFCIVARNPVSNNFS--SPILARKLCEGAADP 222
DB 179 KAGTHPLNPANSHLLSLTLGPQHADNIYICTVSNPISNNSTQTFSP-----WPGCRTPD 232
QY 223 DSSM-----VLLCLLVPLLLSLFLVLGLFWLFLKRRQBEYIE---EKRVDIC 268
DB 233 SETKPVAVYAGLGGVIMILIMVILQ-----LRRGKTNHYQTTVEKKSLLTY 281
QY 269 RETPNTCPHSGENTYDTPHTNRTILKEDPANTVY--STVEIPKQKNPHSL-----LT 321
DB 282 AQVQKEGP---LQKLDSEF-----AQDPCTIIVAAATEPVPSVQETNSITVYASVT 331
QY 322 MPDT 325
:|:|:

DB 332 LPES 335
RESULT 9
US-08-880-875-2
Sequence 2, Application US/08880875
Patent No. 6399065
GENERAL INFORMATION:
APPLICANT: Aversa, Gregorio
APPLICANT: Chang, Chia-Chun J.
APPLICANT: Cocks, Benjamin G.
APPLICANT: de Vries, Jan E.
TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
TITLE OF INVENTION: SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,777
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/348,792
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0436K
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-875-2
Query Match 10.3%; Score 182.5; DB 4; Length 335;
Best Local Similarity 22.5%; Pred. No. 4.8e-11;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;
QY 8 LTIYILM-QLTGSASGP-----VKELVSGVGAVTPPL-----KSKVKQVDSIVWT 54
DB 7 LSLTFVLFLAFGASGTGGRMMNCPKILRQLGSKVLLPLTYERINKSMNKSIIHVMT 66
QY 55 FNT-----TPLVITQP-EGGTIIVTQNRNRVDFPDGGYSILKSLKKNDSGIYVGI 107
DB 67 AKLSLENVENKIVSLDPSEAG-----PPRYLGRYKYLENLTLGIRSRKDEGWYLMTL 122
QY 108 YSS-SLQQPSTQBYLVHVTYHLKSKPTMTGLOSNGKTCVTNLTCCMEHGEDVIYTW-- 164
DB 123 EKNVSQVRCFLQ---LRLYEQVSTPEIKVLNKTQENGCTLLIGCTVEKGDH-VAYSNSE 178
QY 165 KALQQAANSHNGSILPISWRNGESDMTFCIVARNPVSNNFS--SPILARKLCEGAADP 222
DB 179 KAGTHPLNPANSHLLSLTLGPQHADNIYICTVSNPISNNSTQTFSP-----WPGCRTPD 232
QY 223 DSSM-----VLLCLLVPLLLSLFLVLGLFWLFLKRRQBEYIE---EKRVDIC 268
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Db      233  SETKPWAVAGLLGGVIMILMVILQ-----LRRGKTNHYQTVEKSLITY 281
Qy      269  RETPNICPHSGENTYDTIPIHNRILKEDPANTWY--STVEIPKKNENPHSL-----LT 321
Db      282  AQVKQKGP--LQKKLDSFP-----AQDECTIYVAATEPVESVQETNSITTVVASVT 331
Qy      322  MPDT 325
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Db      332  LPES 335

RESULT 10
US-09-369-248A-3
; Sequence 3, Application US/09369248A
; Patent No. 6620912
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Dendritic Enriched Secreted Lymphocyte Activation
; TITLE OF INVENTION: Molecule
; FILE REFERENCE: PF448P1
; CURRENT APPLICATION NUMBER: US/09/369 248A

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Query Match	10.3%;	Score 182.5;	DB 4;	Length 335;
Best Local Similarity	22.5%;	Pred. No. 4.8e-11;		
Matches	82;	Conservative 72;	Mismatches 129;	Indels 81;
				Gaps 19;
QY	8	LTLVILW-QLTGSAAGP-----VKELVSGVGAVTPPL-----KSKVQVDIVYVT	54	
Db	7	LSLTFVLFLAFGASVYTCGRMNCFKILRLQSGKVLPLPLTYERINKSMNKSIHIVTM	66	
QY	55	FNT-----TPLVIQIP-EGGTIVQNRNRVDFPDGGYSLKSLKKNDSGIYYVGI	107	
Db	67	AKSLENSVENKIVSLDPSEAG---PPRYLGDRYKYLENLTLGIRSKEDGEGWYMTL	122	
QY	108	YSS-SLQPPSTQEVYLVHVLHSLKPKVTWGLQSNKNGTCVTNLTCCMEHGSDVIYTW--	164	
Db	123	EXNVSQRFCLQ---LRLYEOVSTPEIKVLNKTQENGCTLTLCGTVEKGDH-VAYSWE	178	
QY	165	KALGOANESHGSLPISWRGESDMTFTICVARNPVRNFS--SPILARKLCEGAADP	222	
Db	179	KAGTHPLNPANSHLSLTLPQHADNIYICTVSNPISNNSQTFFP-----WPCRTDP	232	
QY	223	DSSM-----VLLCLLLVPLLISUEVLGLFLWFLKRRQBEYTE---EKQRVDIC	268	
Db	233	SETKPWAVYAGLLGGVIMILMVILQ-----LRRRGKTNHYQTTVEKKSITIY	281	
QY	269	RETENICPHSGENTGYDTIPIHTNRTILKEDPANTVY--STVEIPKKMENPISL-----LT	321	
Db	282	AQVKQGP--LQKLDSP-----AQDCTTIYVAATEPVPVSQVETNSITYASVT	331	
QY	322	MPDT 325		
Db	332	LPES 335		

RESULT 11
US-08-348-792-8
; Sequence 8, Application US/08348792
; Patent No. 5576423
; GENERAL INFORMATION:

APPLICANT: Aversa, Gregorio
 APPLICANT: Chang, Chia-Chun J.
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: de Vries, Jan E.
 TITLE OF INVENTION: PURIFIED GENES ENCODING MAMMALIAN CELL
 SURFACE ANTIGENS; PROTEINS AND ANTIBODIES
 TITLE OF INVENTION: 12
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/348,792
 FILING DATE: 02-DEC-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0436
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 307 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-348-792-8

Query Match	10.2%	Score 180;	DB 1;	Length 307;
Best Local Similarity	22.6%;	Pred. No. 7.8e-11;		
Matches	76;	Conservative 67;	Mismatches 120;	Indels 74; Gaps 17;
QY	28	ELVGSVGGATPEFL-----KSKVKQVDSIVTWFTNT-----TPLYTIQIP-EGGTIIIVTQ	74	
Db	6	KILRQIGSKVLLPETYTERINKSNMKSITHIVTWAKLSLENSVENKIVSLDPSEAG-----PP	61	
QY	75	NNRNRVDFPDGCGYSKLKSLKKNDSGIYVVGIYSS--SLOQPSTQEVLYHWYHLSPKV	133	
Db	62	RYLGDYKVFYLENLTLGIRESRKDEDEGWYMLTLEKNVSVQRFCLQ---LRLYEQVSTPEI	118	
QY	134	TMGLQNKQGTCTVNNITCCMEHGEEDVIYTW--KALGQAAENSHSGSILPISRWGSESDM	191	
Db	119	KVLNKTQENGCTCLILGCTVEKGDH-VAYSWSSEKAGTHPLNPANSHLLSLTLGPQHADN	177	
QY	192	TFICVARNPVSRNFS--SPILARKLCEGAADDPDSM-----VLLCLLLVPLLL	238	
Db	178	IYICTVSNPISNNSTQFSP-----WPGCRTDSETKPMAYAGLGGVIMILIMVYILQ	231	
QY	239	SFLVGLGLFLWFKRREQEYIE---EKKKRVDCIRETPNICPHSGENTGYDTIPIHTNRTIL	295	
Db	232	-----LERRKTHNYQTTVEKKSITVYAQVKQKGP---LQKLDSPF-----	270	
QY	296	KGDGPANTVY--STVEIPKKNMNPHSI-----LTMPDT	325	
Db	271	ADDPCTTIYVAATEPVPVPSVOENSTNITVYASVTLPES	307	

RESULT 12
US-08-462-738-8
; Sequence 8, Application US/08462738
; Patent No. 5977303
; GENERAL INFORMATION:
; APPLICANT: Aversa, Gregorio

Db 263 KLDSP-----AQDPCTIIVATEPVPEVSQETNSITVYASVTLPE 305

Search completed: August 18, 2004, 15:45:20
Job time : 22 secs

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Result No.	Score	Query			DB	ID	Description
		Match	Length	Count			
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2	182.5	10.3	335	2	S58892	signaling lymphocy	
3	144	8.1	344	2	B28967	T-cell surface gly	
4	138	7.8	344	2	I45985	CD2 antigen protei	
5	136.5	7.7	351	1	RWUC2	T-cell surface gly	
6	134	7.6	240	2	S01299	OX-42 membrane gly	
7	130	7.3	344	1	RWRT2	T-cell surface gly	
8	126.5	7.1	240	2	JL0143	antigen BCM1 precu	
9	125.5	7.1	321	2	JH0395	biliary glycoprote	
10	125.5	7.1	351	2	JH0396	biliary glycoprote	
11	125.5	7.1	417	2	JH0394	biliary glycoprote	
12	125.5	7.1	464	2	C30127	transmembrane car	
13	124.5	7.1	526	1	A32164	biliary glycoprote	
14	124.5	7.0	344	2	A27681	nonspecific cross-	
15	122.5	6.9	521	2	S34338	biliary glycoprote	
16	119	6.7	458	2	JC3509	biliary glycoprote	
17	114.5	6.5	702	2	A36319	carcinoembryonic a	
18	113.5	6.4	458	1	WMMSR1	biliary glycoprote	
19	113.5	6.4	521	2	JC3508	biliary glycoprote	
20	109.5	6.2	432	2	S30193	T-cell surface gly	
21	108.5	6.1	365	2	JC7780	coxsackie- and ade	
22	107.5	6.1	398	2	I49443	gene B24 protein -	
23	106	6.0	897	2	G84613	hypothetical prote	
24	105.5	6.0	329	1	A48754	B7-2 antigen - hum	
25	104	5.9	349	2	A34815	carcinoembryonic a	
26	102.5	5.8	458	2	S23969	cell-adhesion mole	
27	102.5	5.8	526	2	A37821	butyrophilin - bov	
28	101.5	5.7	761	2	T00940	hypothetical prote	
29	101	5.7	587	2	JH0464	DM-GRASP precursor	

103	86	4.9	212	2	C33258	176	80	4.5	1040	2	A49356	transient axonal g
104	86	4.9	354	1	VBEB67	177	80	4.5	1170	2	A40558	thrombospondin 1 p
105	86	4.9	428	2	I57486	178	79.5	4.5	1134	2	I46627	rearranged T-cell
106	86	4.9	885	2	B86257	179	79.5	4.5	249	1	A61087	myelin P0 glycopro
107	86	4.9	1327	2	T09402	180	79.5	4.5	273	2	B28928	pregnancy-specific
108	85.5	4.8	324	2	G43354	181	79.5	4.5	275	2	A28928	pregnancy-specific
109	85.5	4.8	326	2	F43354	182	79.5	4.5	282	2	C28928	pregnancy-specific
110	85.5	4.8	333	2	A43354	183	79.5	4.5	289	2	G90314	oxidoreductase lim
111	85.5	4.8	335	2	H43354	184	79.5	4.5	338	2	JQ1121	cysteine proteinas
112	85.5	4.8	941	1	TVMMD	185	79.5	4.5	400	2	A10104	probable galactosi
113	85.5	4.8	2588	2	T14342	186	79.5	4.5	430	2	T28143	tapasin 1 homolog,
114	85	4.8	428	2	JS0032	187	79.5	4.5	446	2	T34782	probable signal pe
115	85	4.8	731	2	T16524	188	79.5	4.5	490	2	I41293	ECOE type I restri
116	85	4.8	757	1	S48841	189	79.5	4.5	769	2	S16236	fibroblast growth
117	84.5	4.8	656	2	A96724	190	79.5	4.5	822	2	A45081	keratinocyte growt
118	84	4.7	275	2	JC7604	191	79.5	4.5	822	2	A41794	keratinocyte growt
119	84	4.7	851	2	D90216	192	79.5	4.5	873	1	I48952	VLDR receptor prec
120	84	4.7	1379	1	S01254	193	79.5	4.5	980	1	TVCTMD	macrophage colony-
121	84	4.7	1499	2	I50212	194	79.5	4.5	1465	2	S43529	165K protein, skel
122	84	4.7	3034	2	T14119	195	79.5	4.5	2491	1	A28372	insulin-like growt
123	83.5	4.7	315	2	H71009	196	79	4.5	210	2	C87256	hypothetical prote
124	83.5	4.7	392	2	T33444	197	79	4.5	244	2	AC1765	B. subtilis TagA p
125	83.5	4.7	656	2	B49423	198	79	4.5	438	2	G64513	hypothetical prote
126	83.5	4.7	775	2	T21436	199	79	4.5	479	2	G84099	carboxy-terminal p
127	83.5	4.7	1501	2	I58148	200	79	4.5	584	2	T08678	hypothetical prote
128	83.5	4.7	1863	2	S45217	201	79	4.5	657	2	S77543	short-chain alchoh
129	83	4.7	335	2	A33514	202	79	4.5	903	2	T20804	hypothetical prote
130	83	4.7	757	2	I45956	203	79	4.5	1228	2	G96751	hypothetical prote
131	83	4.7	873	1	A49729	204	79	4.5	1361	2	T30884	neural specific DN
132	83	4.7	925	2	T34745	205	78.5	4.4	235	2	S25750	ig lambda chain -
133	83	4.7	1106	2	S59782	206	78.5	4.4	429	1	EHRT	ig epsilon chain C
134	83	4.7	2489	2	S96780	207	78.5	4.4	497	2	C91225	probable oxidoredu
135	82.5	4.7	393	2	B36203	208	78.5	4.4	497	2	A86072	probable oxidoredu
136	82.5	4.7	826	2	A71617	209	78.5	4.4	539	2	T01513	Ctp synthase (EC 6
137	82.5	4.7	1004	2	A71617	210	78.5	4.4	588	2	I37202	B-CAM protein - hu
138	82.5	4.7	2626	1	I38344	211	78.5	4.4	628	2	I38000	Lutheran blood gro
139	82	4.6	386	2	B69666	212	78.5	4.4	638	2	T51383	receptor protein k
140	82	4.6	609	2	S43009	213	78.5	4.4	831	2	S39835	hypothetical prote
141	82	4.6	680	2	B53743	214	78.5	4.4	847	2	JH0371	B-cell adhesion pr
142	82	4.6	3562	2	A47171	215	78.5	4.4	1036	2	S22383	axonin 1 precursor
143	81.5	4.6	278	1	TDRTOX	216	78.5	4.4	1038	2	AG2187	hypothetical prote
144	81.5	4.6	352	2	I77374	217	78.5	4.4	1468	2	T05672	hypothetical prote
145	81.5	4.6	355	2	T06122	218	78	4.4	257	2	A97121	undecaprenyl pyrop
146	81.5	4.6	378	2	S00842	219	78	4.4	272	2	I48268	biliary glycoprote
147	81.5	4.6	497	2	D97264	220	78	4.4	286	2	A28333	carcinoembryonic a
148	81.5	4.6	524	2	S44982	221	78	4.4	335	2	C54312	pregnancy-specific
149	81.5	4.6	708	2	T48022	222	78	4.4	402	2	T09062	probable advanced
150	81	4.6	335	2	B33251	223	78	4.4	490	2	T43184	probable box ATP-dep
151	81	4.6	338	2	JC4776	224	78	4.4	604	2	T41249	DEAD box ATP-dep
152	81	4.6	374	2	S57750	225	78	4.4	608	2	AB3562	gtp-binding protei
153	81	4.6	760	2	S19374	226	78	4.4	609	1	HMNZKA	hemagglutinin - ri
154	81	4.6	769	2	E97092	227	78	4.4	761	1	IJHUNG	neural cell adhesi
155	81	4.6	829	1	IJHUCP	228	78	4.4	836	2	T42323	hypothetical prote
156	81	4.6	1898	2	S46216	229	78	4.4	905	2	S43084	probable vacuolar
157	81	4.6	1941	2	T30554	230	78	4.4	905	2	T38314	hypothetical prote
158	80.5	4.5	346	2	S46993	231	77.5	4.4	172	2	T34227	conserved hypothet
159	80.5	4.5	376	2	B85435	232	77.5	4.4	214	2	C89833	CD8 alpha-chain -
160	80.5	4.5	462	2	H97292	233	77.5	4.4	236	2	T41012	SHP substrate-1 pr
161	80.5	4.5	473	2	AG0612	234	77.5	4.4	248	2	I46082	SHP substrate-1 pr
162	80.5	4.5	475	2	I76668	235	77.5	4.4	509	2	JC5288	F12G12.2 protein -
163	80.5	4.5	540	2	H90751	236	77.5	4.4	539	2	JC5289	gluconate dehydrog
164	80.5	4.5	540	2	B85615	237	77.5	4.4	591	2	H83362	ferrienterobactin-
165	80.5	4.5	540	2	B64829	238	77.5	4.4	717	2	AD3097	ferrienterobactin-
166	80.5	4.5	721	2	T09631	239	77.5	4.4	717	2	E38189	vascular cell adhe
167	80.5	4.5	823	2	T08092	240	77.5	4.4	717	2	E38189	vascular cell adhe
168	80.5	4.5	3343	2	S44887	241	77.5	4.4	739	2	A41288	dynammin-related pr
169	80.5	4.5	6642	2	T29757	242	77.5	4.4	863	2	S64742	neuraxin - rat
170	80	4.5	307	1	RWMSBC	243	77.5	4.4	881	2	S06017	env protein - huma
171	80	4.5	341	2	I61725	244	77.5	4.4	881	2	S03068	hypothetical prote
172	80	4.5	343	2	G90680	245	77.5	4.4	968	2	T25667	polynucleotide pho
173	80	4.5	343	2	C85531	246	77.5	4.4	991	2	T48631	hypothetical prote
174	80	4.5	454	2	A46532	247	77.5	4.4	1015	2	T32186	hypothetical prote
175	80	4.5	482	2	JH0110	248	77.5	4.4				

249	77.5	4.4	1099	2	T18713	hypothetical prote	322	76	4.3	1018	2	JC4211	neural adhesion pr
250	77.5	4.4	1205	2	T13959	timeless protein T	323	76	4.3	1093	2	T51503	valine-tRNA ligase
251	77.5	4.4	1262	1	B49758	protein-tyrosine p	324	76	4.3	2029	1	TDFFLK	protein-tyrosine-p
252	77.5	4.4	1496	1	A48758	protein-tyrosine-p	325	75.5	4.3	246	2	A47712	myelin/oligodendro
253	77.5	4.4	1894	2	C54689	protein-tyrosine-p	326	75.5	4.3	326	2	JC4124	pregnancy-specific
254	77.5	4.4	1912	2	A56178	protein-tyrosine-p	327	75.5	4.3	419	2	S42989	T48 protein - frui
255	77.5	4.4	12332	2	S12332	ubiquitin-protein	328	75.5	4.3	432	2	T40614	G beta repeat prot
256	77	4.3	327	2	S06611	Ig gamma-2 chain C	329	75.5	4.3	421	2	T30130	hypothetical prote
257	77	4.3	328	2	I47158	Ig gamma 1 chain c	330	75.5	4.3	446	2	A95140	exodeoxyribonuclea
258	77	4.3	328	2	JC5519	50K glycoprotein p	331	75.5	4.3	462	2	A84689	chloroplast membra
259	77	4.3	398	2	B85353	protein F2E2.6 [im	332	75.5	4.3	485	2	T28076	hypothetical prote
260	77	4.3	439	2	S51378	probable membrane	333	75.5	4.3	819	2	T85744	hypothetical prote
261	77	4.3	491	2	JE0276	voltage-gated pota	334	75.5	4.3	933	2	H89045	hypothetical prote
262	77	4.3	502	2	S61935	SKS1 protein - yea	335	75.5	4.3	1020	2	S05944	neuroanal cell surr
263	77	4.3	523	2	T05946	cytochrome P450 78	336	75.5	4.3	2109	1	I50421	aggronan precursor
264	77	4.3	796	2	JC7966	xylan 1,4-beta-xy	337	75	4.2	150	2	D95131	hypothetical prote
265	77	4.3	873	1	QR8VD	VLDL receptor prec	338	75	4.2	208	2	D71529	probable anthranil
266	77	4.3	1021	2	I3207	leukocyte surface	339	75	4.2	466	2	D84906	probable beta-keo
267	77	4.3	1029	2	D83120	probable RND efflu	340	75	4.2	491	2	AC2650	glucose-6-phosphat
268	77	4.3	1041	2	S55862	probable membrane	341	75	4.2	503	2	B97432	glucose-6-phosphat
269	77	4.3	1897	1	TDHULK	leukocyte antigen-	342	75	4.2	543	2	S26609	glutamate/aspartat
270	77	4.3	2167	2	AF1489	cell wall-associat	343	75	4.2	572	2	B46529	Ig Y heavy chain (
271	77	4.3	4836	2	T14346	herc2 protein - mo	344	75	4.2	573	2	S12838	Ig mu chain precu
272	76.5	4.3	177	1	C40428	nonspecific cross-	345	75	4.2	622	2	B86751	hypothetical prote
273	76.5	4.3	191	2	E75132	molybdopterin-guan	346	75	4.2	686	2	A55665	microtubule-associ
274	76.5	4.3	238	2	T24314	hypothetical prote	347	75	4.2	747	1	QRECFE	ferrichrome-iron r
275	76.5	4.3	251	2	S75312	hypothetical prote	348	75	4.2	747	2	B85499	outer membrane rec
276	76.5	4.3	296	2	G82131	conserved hypothet	349	75	4.2	747	2	B90648	outer membrane rec
277	76.5	4.3	390	2	D86291	hypothetical prote	350	75	4.2	821	1	TWMSBK	fibroblast growth
278	76.5	4.3	394	2	S20905	hypothetical prote	351	75	4.2	976	1	TWMSMD	macrophage colony-
279	76.5	4.3	402	2	A54312	pregnancy-specific	352	75	4.2	1091	1	IUCHNL	neural cell adhesi
280	76.5	4.3	423	2	AB1142	N-carbamyl-L-amino	353	75	4.2	1256	2	T03096	neural cell adhesi
281	76.5	4.3	426	2	S09016	pregnancy-specific	354	75	4.2	1338	2	T02206	hypothetical prote
282	76.5	4.3	426	2	C55181	pregnancy-specific	355	75	4.2	1338	2	I38346	hypothetical prote
283	76.5	4.3	426	2	B35334	pregnancy-specific	356	74.5	4.2	232	1	DXCH	elastin titin - hu
284	76.5	4.3	436	2	A55181	pregnancy-specific	357	74.5	4.2	278	2	A39037	ovalbumin-related
285	76.5	4.3	495	2	A55181	pregnancy-specific	358	74.5	4.2	278	2	A39037	carcinoembryonic a
286	76.5	4.3	497	2	D65189	YigC protein - Esc	359	74.5	4.2	309	2	T31908	hypothetical prote
287	76.5	4.3	582	2	A71906	DNA polymerase III	360	74.5	4.2	321	2	S10006	hypothetical prote
288	76.5	4.3	727	2	T23585	hypothetical prote	361	74.5	4.2	379	2	B55522	lipoprotein D prec
289	76.5	4.3	788	2	S17906	hypothetical prote	362	74.5	4.2	379	2	D91078	probable lipoprote
290	76.5	4.3	839	2	B96538	hypothetical prote	363	74.5	4.2	379	2	E85923	lipoprotein (impor
291	76.5	4.3	876	2	S71277	hypothetical prote	364	74.5	4.2	463	2	T14884	hypothetical prote
292	76.5	4.3	876	2	D85350	serine/threonine-s	365	74.5	4.2	518	2	D69539	conserved hypothet
293	76.5	4.3	1005	2	T18537	hypothetical prote	366	74.5	4.2	544	2	I51593	protein-tyrosine k
294	76.5	4.3	1043	2	T19734	Ig heavy chain - c	367	74.5	4.2	688	2	A47705	triacylglycerol li
295	76.5	4.3	1071	2	T18307	hypothetical prote	368	74.5	4.2	705	2	S1635	fibroblast growth
296	76.5	4.3	1089	1	PFHUGA	suppressor protein	369	74.5	4.2	741	2	F90739	probable transport
297	76.5	4.3	1124	2	JX0293	platelet-derived g	370	74.5	4.2	741	2	H85589	probable transport
298	76.5	4.3	1154	2	A56242	E-box-binding repr	371	74.5	4.2	764	2	A49448	irregular chiasm C
299	76.5	4.3	1328	2	S62467	ATP-dependent DNA	372	74.5	4.2	771	2	T34376	hypothetical prote
300	76.5	4.3	1461	2	B70588	probable polyketid	373	74.5	4.2	786	2	H64817	probable membrane
301	76.5	4.3	1802	2	S69703	HKRI protein precu	374	74.5	4.2	795	2	T20609	hypothetical prote
302	76.5	4.3	2039	2	T15347	ankyrin-related un	375	74.5	4.2	889	1	VCLJG5	env polyprotein -
303	76	4.3	138	2	AH1172	phosphosystem I prot	376	74.5	4.2	884	2	T00326	hypothetical prote
304	76	4.3	144	2	S49449	Ig lambda chain -	377	74.5	4.2	1003	2	T19638	hypothetical prote
305	76	4.3	230	2	T23147	hypothetical prote	378	74.5	4.2	1007	2	PN0156	glutamate receptor
306	76	4.3	262	2	A64882	probable carboxype	379	74.5	4.2	1008	2	S28858	glutamate receptor
307	76	4.3	262	2	A99867	probable carboxype	380	74.5	4.2	1178	2	E87145	contactin precursor
308	76	4.3	262	2	H85751	prephenate dehydro	381	74.5	4.2	1179	2	S31145	[beta] subunit of
309	76	4.3	262	2	H85751	conserved hypothet	382	74.5	4.2	1522	2	T00028	DNA-directed RNA p
310	76	4.3	285	2	B97010	amalgam protein pr	383	74.5	4.2	1522	2	T00028	brain-specific ang
311	76	4.3	306	2	H69759	brevican precursor	384	74.5	4.2	1896	2	T08851	receptor DEC-205 -
312	76	4.3	333	2	A31923	DNA-directed DNA p	385	74.5	4.2	2256	2	AD1018	Down syndrome cell
313	76	4.3	378	2	I46268	hypothetical prote	386	74.5	4.2	2364	2	A56577	large repetitive p
314	76	4.3	487	1	S55194	L-asparagine perme	387	74.5	4.2	2783	2	T34416	microtubule-associ
315	76	4.3	507	2	T47021	hypothetical prote	388	74	4.2	203	2	S36291	hypothetical prote
316	76	4.3	508	2	AD0236	hypothetical prote	389	74	4.2	234	2	S01320	T-cell receptor ga
317	76	4.3	550	2	G90497	hypothetical prote	390	74	4.2	278	2	JC1506	Ig kappa chain pre
318	76	4.3	758	2	T15577	hypothetical prote	391	74	4.2	278	2	JC1506	biliary glycoprote
319	76	4.3	841	2	T01011	hypothetical prote	392	74	4.2	333	2	PS0018	Ig gamma-2b chain
320	76	4.3	964	2	T15746	hypothetical prote	393	74	4.2	334	2	T19637	hypothetical prote
321	76	4.3	978	2	S16385	macrophage colony-	394	74	4.2	349	2	S68092	protein-glutamine
										384	2	H64161	hypothetical prote

395	74	4.2	403	2	I52590	m33-B isoform - mo	468	72.5	4.1	202	2	S36293	T-cell receptor ga
396	74	4.2	424	2	T43498	hypothetical prote	469	72.5	4.1	221	2	T31620	hypothetical prote
397	74	4.2	463	2	C69997	probable proline t	470	72.5	4.1	334	2	G01650	malate dehydrogena
398	74	4.2	468	2	S70297	SPS2 protein homol	471	72.5	4.1	336	2	C27658	pregnancy-specific
399	74	4.2	502	2	T40792	hypothetical prote	472	72.5	4.1	351	2	AG1729	protein gp19 (Bact
400	74	4.2	548	2	A44302	protein-glutamine	473	72.5	4.1	352	2	B34595	pregnancy-specific
401	74	4.2	586	2	T15259	hypothetical prote	474	72.5	4.1	363	2	I39726	mannopine biosynth
402	74	4.2	611	2	F82442	hypothetical prote	475	72.5	4.1	371	2	T40287	hypothetical prote
403	74	4.2	645	2	T39614	probable peptide A	476	72.5	4.1	371	2	B90437	hypothetical prote
404	74	4.2	673	2	T48701	kinase-binding pro	477	72.5	4.1	399	2	A11114	surface protein (p
405	74	4.2	860	2	JC5702	hypothetical prote	478	72.5	4.1	424	2	A34595	pregnancy-specific
406	74	4.2	862	2	I49583	ErB kinase activa	479	72.5	4.1	435	2	D33258	tyA protein - yeas
407	74	4.2	876	2	B96693	differentiation an	480	72.5	4.1	440	2	S22895	tyA protein - yeas
408	74	4.2	900	2	G96617	probable receptor	481	72.5	4.1	440	2	A83294	tyA protein - yeas
409	74	4.2	1063	2	A33830	probable disease r	482	72.5	4.1	478	2	A49228	trypsin-like prote
410	74	4.2	1063	2	JC4700	cation efflux syst	483	72.5	4.1	478	2	A11146	hypothetical cell
411	74	4.2	1130	2	T23104	cadmium, zinc, cob	484	72.5	4.1	491	2	T22844	hypothetical prote
412	74	4.2	1133	2	T23103	hypothetical prote	485	72.5	4.1	527	2	D75127	hypothetical prote
413	74	4.2	1165	1	S45879	hypothetical prote	486	72.5	4.1	527	2	D75127	hypothetical prote
414	74	4.2	1237	2	E86457	chitin synthase (E	487	72.5	4.1	666	2	A39610	SLX1 protein - yea
415	74	4.2	1367	2	T33819	probable RNA helic	488	72.5	4.1	682	2	A35969	heparin-binding gr
416	74	4.2	1482	2	T15308	hypothetical prote	489	72.5	4.1	682	2	T39838	hypothetical prote
417	74	4.2	1482	2	T15308	hypothetical prote	490	72.5	4.1	769	2	JC7352	glucose-regulated
418	74	4.2	1482	2	T15308	hypothetical prote	491	72.5	4.1	769	2	T45854	hypothetical prote
419	74	4.2	1482	2	T15308	hypothetical prote	492	72.5	4.1	842	2	E96641	hypothetical prote
420	73.5	4.1	325	2	S49451	HC-toxin synthetas	493	72.5	4.1	851	2	S44890	nc1-1 ZK112.2 prot
421	73.5	4.1	364	2	A30521	projectin - fruit	494	72.5	4.1	876	2	A49508	protein-tyrosine k
422	73.5	4.1	428	2	B39667	cysteine proteinas	495	72.5	4.1	895	2	T11979	Preprotein translo
423	73.5	4.1	447	2	T33773	myeloid cell surfa	496	72.5	4.1	913	2	A48280	receptor tyrosine
424	73.5	4.1	740	2	AH0600	dihydrootase pyr	497	72.5	4.1	1057	2	S45801	probable membrane
425	73.5	4.1	797	2	T27518	hypothetical prote	498	72.5	4.1	1123	2	A80125	exodeoxyribonuclea
426	73.5	4.1	850	2	JC5700	hypothetical prote	499	72.5	4.1	1138	2	A82939	membrane nucleasa
427	73.5	4.1	880	1	VCLJ52	ErB kinase activa	500	72.5	4.1	1272	2	S26180	neurofascin - chic
428	73.5	4.1	923	2	F84732	env polypeptid pr	501	72.5	4.1	1434	2	T30172	transmembrane prot
429	73.5	4.1	926	2	D83688	probable ligand-ga	502	72.5	4.1	1575	2	T18545	lysobactin synthet
430	73.5	4.1	957	2	C69463	glucan 1,4-beta-gl	503	72.5	4.1	1575	2	T18545	lysobactin synthet
431	73.5	4.1	1166	2	S37692	type I restriction	504	72.5	4.1	1575	2	T18545	lysobactin synthet
432	73.5	4.1	1225	2	T48251	probable tumor sup	505	72.5	4.1	1575	2	T18545	lysobactin synthet
433	73.5	4.1	1240	2	T03097	ubiquitin-protein	506	72.5	4.1	1575	2	T18545	lysobactin synthet
434	73.5	4.1	1240	2	T03097	ubiquitin-protein	507	72.5	4.1	1575	2	T18545	lysobactin synthet
435	73.5	4.1	2042	2	AD1129	probable peptidogl	508	72.5	4.1	1575	2	T18545	lysobactin synthet
436	73.5	4.1	2301	1	GNNYTN	variant-specific s	509	72.5	4.1	1575	2	T18545	lysobactin synthet
437	73.5	4.1	3255	2	G81702	genome polypeptid	510	72.5	4.1	1575	2	T18545	lysobactin synthet
438	73.5	4.1	4544	1	S02392	adherence factor T	511	72.5	4.1	1575	2	T18545	lysobactin synthet
439	73	4.1	147	2	T34265	alpha-2-macroglobu	512	72.5	4.1	1575	2	T18545	lysobactin synthet
440	73	4.1	220	1	G69047	hypothetical prote	513	72.5	4.1	1575	2	T18545	lysobactin synthet
441	73	4.1	235	2	S14675	conserved hypotet	514	72.5	4.1	1575	2	T18545	lysobactin synthet
442	73	4.1	250	2	S27544	ig lambda chain -	515	72.5	4.1	1575	2	T18545	lysobactin synthet
443	73	4.1	293	2	H96906	hypothetical prote	516	72.5	4.1	1575	2	T18545	lysobactin synthet
444	73	4.1	322	2	H84095	hypothetical prote	517	72.5	4.1	1575	2	T18545	lysobactin synthet
445	73	4.1	354	2	T27112	hypothetical prote	518	72.5	4.1	1575	2	T18545	lysobactin synthet
446	73	4.1	389	2	T46722	conserved hypotet	519	72.5	4.1	1575	2	T18545	lysobactin synthet
447	73	4.1	397	2	E86304	F611.9 protein - A	520	72.5	4.1	1575	2	T18545	lysobactin synthet
448	73	4.1	413	2	S65948	hemolin - cecropia	521	72.5	4.1	1575	2	T18545	lysobactin synthet
449	73	4.1	413	2	S38921	hemolin precursor	522	72.5	4.1	1575	2	T18545	lysobactin synthet
450	73	4.1	432	1	RMQQT4	T-cell surface gly	523	72.5	4.1	1575	2	T18545	lysobactin synthet
451	73	4.1	476	2	H84524	probable fatty aci	524	72.5	4.1	1575	2	T18545	lysobactin synthet
452	73	4.1	519	2	S38921	hypothetical prote	525	72.5	4.1	1575	2	T18545	lysobactin synthet
453	73	4.1	590	2	I56526	interleukin 1 rece	526	72.5	4.1	1575	2	T18545	lysobactin synthet
454	73	4.1	666	1	A36026	kinasin-related pr	527	72.5	4.1	1575	2	T18545	lysobactin synthet
455	73	4.1	730	2	S64998	hypothetical prote	528	72.5	4.1	1575	2	T18545	lysobactin synthet
456	73	4.1	735	2	T00850	probable receptor-	529	72.5	4.1	1575	2	T18545	lysobactin synthet
457	73	4.1	853	1	IJBONC	neural cell adhesi	530	72.5	4.1	1575	2	T18545	lysobactin synthet
458	73	4.1	864	2	JH0438	penicillin-binding	531	72.5	4.1	1575	2	T18545	lysobactin synthet
459	73	4.1	901	1	P3XR17	core protein VP3 -	532	72.5	4.1	1575	2	T18545	lysobactin synthet
460	73	4.1	1014	2	T13476	hypothetical prote	533	72.5	4.1	1575	2	T18545	lysobactin synthet
461	73	4.1	1072	2	A38457	integrin alpha-6 c	534	72.5	4.1	1575	2	T18545	lysobactin synthet
462	73	4.1	1171	2	T31635	hypothetical prote	535	72.5	4.1	1575	2	T18545	lysobactin synthet
463	73	4.1	1179	2	T05673	hypothetical prote	536	72.5	4.1	1575	2	T18545	lysobactin synthet
464	73	4.1	1515	1	S51863	cadmium resistance	537	72.5	4.1	1575	2	T18545	lysobactin synthet
465	73	4.1	1737	2	A59235	unconventional myo	538	72.5	4.1	1575	2	T18545	lysobactin synthet
466	73	4.1	1806	2	T33298	hypothetical prote	539	72.5	4.1	1575	2	T18545	lysobactin synthet
467	73	4.1	3788	2	T30851	lysosomal traffick	540	72.5	4.1	1575	2	T18545	lysobactin synthet

T-cell receptor ga
hypothetical prote
malate dehydrogena
pregnancy-specific
protein gp19 (Bact
pregnancy-specific
mannopine biosynth
hypothetical prote
hypothetical prote
surface protein (p
pregnancy-specific
tyA protein - yeas
tyA protein - yeas
trypsin-like prote
hypothetical cell
hypothetical prote
hypothetical prote
SLX1 protein - yea
heparin-binding gr
hypothetical prote
glucose-regulated
hypothetical prote
nc1-1 ZK112.2 prot
protein-tyrosine k
Preprotein translo
receptor tyrosine
probable membrane
exodeoxyribonuclea
membrane nucleasa
neurofascin - chic
transmembrane prot
lysobactin synthet
dynein heavy chain
probable peptide s
hypothetical prote
purine nucleoside
hypothetical prote
scarcrow-like pro
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
gamma-aminobutyrat
two-component sens
probable pseudouri
ABC transporter, p
glutamate transpor
hypothetical prote
hypothetical prote
sensor kinase citA
hypothetical prote
hypothetical prote
hypothetical prote
cell surface glyco
receptor protein k
conserved hypotet
ErB kinase activa
protein F9C16.17 l
P22M8.8 protein -
protein kinase hom
core protein p3 -
androgen receptor
hypothetical prote
hypothetical prote
Smad interacting p
hypothetical prote
sax-3 protein - Ca
vascular endotheli
myosin-light-chain
probable membrane
ryanodine receptor

541	71.5	4.0	145	2	S25743	Ig lambda chain -	614	71	4.0	1251	2	T21389	hypothetical prote
542	71.5	4.0	229	1	B43685	nonstructural prot	615	71	4.0	1338	2	S09982	protein-tyrosine k
543	71.5	4.0	238	4	A49633	Ig lambda-like cha	616	71	4.0	4391	2	A38096	perlecan precursor
544	71.5	4.0	299	2	S50803	hypothetical prote	617	71	4.0	5107	2	T29144	partial CD5 - Caen
545	71.5	4.0	312	2	A64461	hypothetical prote	618	70.5	4.0	203	2	F69381	flagellin (FlaB1-1
546	71.5	4.0	338	2	A64303	conserved hypothet	619	70.5	4.0	223	2	A81068	hypothetical prote
547	71.5	4.0	339	2	S09881	malate dehydrogena	620	70.5	4.0	236	2	D86302	hypothetical prote
548	71.5	4.0	362	2	T05167	hypothetical prote	621	70.5	4.0	246	2	B82764	hypothetical prote
549	71.5	4.0	443	2	T14916	mitosis-specific c	622	70.5	4.0	332	2	T45770	hypothetical prote
550	71.5	4.0	498	2	G90067	malate quinone oxi	623	70.5	4.0	338	1	DBRTMM	malate dehydrogena
551	71.5	4.0	500	2	T11946	ribosomal protein	624	70.5	4.0	358	2	E89588	protein R09F10.8 l
552	71.5	4.0	542	2	AF2587	MFS permease limpo	625	70.5	4.0	429	1	B41902	arsenical pump mem
553	71.5	4.0	542	2	F97369	hypothetical prote	626	70.5	4.0	455	2	G01923	KIR (CI-5) NK rece
554	71.5	4.0	589	2	T50385	hypothetical coile	627	70.5	4.0	502	2	T19108	hypothetical prote
555	71.5	4.0	603	2	H84442	hypothetical prote	628	70.5	4.0	505	2	T15159	hypothetical prote
556	71.5	4.0	669	2	T48466	hypothetical prote	629	70.5	4.0	522	2	T26319	hypothetical prote
557	71.5	4.0	707	2	A54846	fibroblast growth	630	70.5	4.0	526	1	TVFV60	protein-tyrosine k
558	71.5	4.0	707	2	A38429	keratinocyte growt	631	70.5	4.0	533	1	TVCHS	protein-tyrosine k
559	71.5	4.0	764	1	QRHUGS	secretory componen	632	70.5	4.0	537	1	A45501	protein-tyrosine k
560	71.5	4.0	822	2	B54846	fibroblast growth	633	70.5	4.0	545	2	S52313	protein-tyrosine k
561	71.5	4.0	919	2	S33942	hexon protein - hu	634	70.5	4.0	546	2	S52314	protein-tyrosine k
562	71.5	4.0	921	2	F71486	probable yopC/gen	635	70.5	4.0	557	1	TVFVS2	protein-tyrosine k
563	71.5	4.0	1032	2	H64100	acriflavine resist	636	70.5	4.0	558	1	MXRRT	RNA 10 protein - r
564	71.5	4.0	1089	1	S33727	platelet-derived g	637	70.5	4.0	568	1	TVFVS1	protein-tyrosine k
565	71.5	4.0	1180	2	E85719	hypothetical prote	638	70.5	4.0	569	2	A45624	trophozoite cystei
566	71.5	4.0	1348	2	S27812	probable epidermal	639	70.5	4.0	587	1	TVFVPR	protein-tyrosine k
567	71.5	4.0	1348	2	A43917	probable epidermal	640	70.5	4.0	627	2	S14683	Ig mu chain precu
568	71.5	4.0	1374	2	S62524	probable RNA helic	641	70.5	4.0	627	2	A69663	DNA mismatch repai
569	71.5	4.0	1377	2	C70148	DNA-directed RNA p	642	70.5	4.0	630	2	A39344	tumor-associated m
570	71.5	4.0	1413	2	D84481	probable retroelom	643	70.5	4.0	646	2	T48644	negative regulator
571	71.5	4.0	1462	2	T11648	probable mitotic s	644	70.5	4.0	656	2	H84206	acetyl-CoA synthet
572	71.5	4.0	2397	1	A55535	vesicain precursor	645	70.5	4.0	663	1	TVMVR	protein-tyrosine k
573	71	4.0	61	2	G82536	hypothetical prote	646	70.5	4.0	669	2	T13640	probable minor str
574	71	4.0	142	2	S38392	T-cell receptor be	647	70.5	4.0	743	2	F71062	hypothetical prote
575	71	4.0	189	2	G64496	hypothetical prote	648	70.5	4.0	787	2	T41974	replication origin
576	71	4.0	207	2	T50206	hypothetical zinc	649	70.5	4.0	793	2	T41703	dipeptidyl aminope
577	71	4.0	221	2	T21117	hypothetical prote	650	70.5	4.0	844	2	S05988	translation elonga
578	71	4.0	224	2	H81568	conserved hypothet	651	70.5	4.0	877	1	IJBONC	N-cadherin precurs
579	71	4.0	231	2	G72102	ct181 hypothetical	652	70.5	4.0	878	2	S11842	hypothetical prote
580	71	4.0	231	2	B86520	CT181 hypothetical	653	70.5	4.0	895	2	A55413	triglyceride trans
581	71	4.0	258	2	S73803	MG256 homolog H91	654	70.5	4.0	906	1	IUNSCN	N-cadherin precurs
582	71	4.0	329	1	DEDFLM	L-lactate dehydrog	655	70.5	4.0	928	2	G86546	polymorphic oute
583	71	4.0	333	2	AF0407	lipoprotein (impor	656	70.5	4.0	928	2	G81591	polymorphic membra
584	71	4.0	343	2	AI0358	probable fibmbial	657	70.5	4.0	938	2	F86548	polymorphic oute
585	71	4.0	344	2	I56551	neurotrophin - rat	658	70.5	4.0	938	2	H72074	polymorphic membra
586	71	4.0	345	2	I48780	Stral/Epl52 protei	659	70.5	4.0	1088	2	B56715	calcium receptor (
587	71	4.0	346	2	AF1820	sialoglycoproteina	660	70.5	4.0	1200	2	T17404	hyalin - sea urchi
588	71	4.0	387	2	B71611	hypothetical prote	661	70.5	4.0	1356	2	JC1402	protein-tyrosine k
589	71	4.0	389	2	S68155	ubiquinol-cytochro	662	70.5	4.0	1402	2	F84480	probable retroelem
590	71	4.0	390	2	T27033	hypothetical prote	663	70.5	4.0	1427	2	IS1669	tumor suppressor -
591	71	4.0	407	2	T34442	hypothetical prote	664	70.5	4.0	1694	2	S50065	sialoadhesin - mou
592	71	4.0	423	1	EHWS8	Ig epsilon chain C	665	70.5	4.0	2051	2	T30938	receptor tyrosine
593	71	4.0	455	2	S50391	hypothetical prote	666	70.5	4.0	2303	1	GNNYTP	genome polyprotein
594	71	4.0	462	2	JN0719	drought-inducible	667	70.5	4.0	2303	2	S13554	genome polyprotein
595	71	4.0	463	2	AH1758	amino acid transpo	668	70.5	4.0	2464	1	QRMSP1	microtubule-associ
596	71	4.0	509	1	WMVZMX	M9-R protein - myx	669	70.5	4.0	6831	2	A88852	protein unc-22 [im
597	71	4.0	570	2	T11647	probable pyruvate	670	70.5	4.0	6839	2	S57242	twitichin [similar
598	71	4.0	609	2	H82039	GTP-binding protei	671	70.5	4.0	7160	2	T27935	hypothetical prote
599	71	4.0	615	2	S38575	gluconate 2-dehydr	672	70	4.0	115	1	KVNSL6	Ig kappa chain pre
600	71	4.0	682	2	T22064	hypothetical prote	673	70	4.0	203	2	S23043	T-cell receptor ga
601	71	4.0	687	2	A49636	soluble vascular e	674	70	4.0	224	2	I37243	CMRF-35 antigen -
602	71	4.0	690	2	A24545	triacylglycerol li	675	70	4.0	236	2	S25746	Ig lambda chain -
603	71	4.0	691	2	B89797	glycerol ester hyd	676	70	4.0	283	2	AB0105	probable maltodex
604	71	4.0	765	2	E96558	hypothetical prote	677	70	4.0	292	2	T44230	hypothetical prote
605	71	4.0	821	1	TVHUF2	fibroblast growth	678	70	4.0	299	2	D83010	probable binding p
606	71	4.0	876	2	T51507	WD40-repeat protei	679	70	4.0	304	2	G71624	refin PF0025C - m
607	71	4.0	902	1	S54495	probable carrier p	680	70	4.0	347	2	T29415	hypothetical prote
608	71	4.0	940	2	T41992	hypothetical prote	681	70	4.0	356	2	G82938	hemin transport sy
609	71	4.0	956	2	G70327	isoleucine-tRNA li	682	70	4.0	374	2	A46352	ORF1 protein - Chl
610	71	4.0	1018	2	A54744	contactin 1 precu	683	70	4.0	403	2	B36151	tryptophan synthas
611	71	4.0	1027	2	B85089	receptor protein k	684	70	4.0	410	2	I50494	serine proteinase
612	71	4.0	1082	2	S64903	regulatory protein	685	70	4.0	469	2	T46929	hypothetical prote
613	71	4.0	1217	2	T22672	hypothetical prote	686	70	4.0	491	2	T27661	hypothetical prote

687	70	4.0	517	2	T0980	hypothetical prote
688	70	4.0	536	2	T37544	hypothetical serin
689	70	4.0	548	2	E71549	hypothetical prote
690	70	4.0	550	2	T03714	5-epi-aristoloch
691	70	4.0	576	2	A32604	interleukin-1 rece
692	70	4.0	599	2	T48450	hypothetical prote
693	70	4.0	609	2	AE2062	gamma-glutamyltra
694	70	4.0	611	1	W1LEP	El protein - Europ
695	70	4.0	611	2	H70938	probable fad5 pro
696	70	4.0	648	2	T08856	hypothetical prote
697	70	4.0	687	1	A3045	protein-glutamine
698	70	4.0	750	2	T01537	S-receptor kinase
699	70	4.0	805	2	S68441	leptin receptor, s
700	70	4.0	810	1	S57196	calpain (EC 3.4.22

ALIGNMENTS

RESULT 1
A46500
Ly-9.2 antigen - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46500
R:Sandrin, M.S.; Gumley, T.P.; Henning, M.M.; Vaughan, H.A.; Gonez, L.J.; Trapani, J.A.;
J. Immunol. 149, 1636-1641, 1992
A:Title: Isolation and characterization of cDNA clones for mouse Ly-9.
A:Reference number: A46500; MUID:92373005; PMID:1506686
A:Accession: A46500
A>Status: Preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-629 <S>A>
A:Cross-references: GB:M84412; NID:G198931; PIDN:AAA39468.1; PID:G198932
A:Experimental source: C57BL/6
A>Note: sequence extracted from NCBI backbone (NCBIN:111651, NCBIP:111654)
C:Keywords: transmembrane protein

Query Match	19.4%;	Score 343;	DB 2;	Length 629;
Best Local Similarity	29.3%;	Pred. No. 2.2e-20;		
Matches 105;	Conservative 58;	Mismatches 143;	Indels 52;	Gaps 14;

RESULT 2
S58892
signaling lymphocytic activation molecule - human
C.Species: Homo sapiens (man)
C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
C.Accession: S58892

R;Cocks, B.G.; Chang, C.C.; Carballido, J.M.; Yssel, H.; de Vries, J.E.; Aversa, G. Nature 376, 260-263, 1995
A;Title: A novel receptor involved in T-cell activation.
A;Reference number: S58892; MUID:95342241; PMID:7617038
A;Accession: S58892
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-335 <COC>

Query Match	10.3%;	Score 182.5;	DB 2;	Length 335;
Best Local Similarity	22.5%;	Pred. No. 1.9e-07;		
Matches 82;	Conservative 72;	Mismatches 129;	Indels 81;	Gaps 19;

RESULT 3
B28967 T-cell surface glycoprotein CD2 precursor - mouse
N:Alternate names: CD2 antigen; T-lymphocyte antigen CD2; T11 protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1989 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C:Accession: B28967; S01347; S02293
R:RDiamond, D.J.; Clayton, L.K.; Sayre, P.H.; Reinherz, E.L.
Proc. Natl. Acad. Sci. U.S.A. 85, 1615-1619, 1988
A:Title: Exon-intron organization and sequence comparison of human and murine T11 (CD2)
A:Reference number: A28967; MUID:88144486; PMID:2894031
A:Accession: B28967
A:Molecule type: mRNA
A:Residues: 1-344 <DIA>
A:Cross-references: GB:MI19807; NID:g192479; PIDN:AAA37393.1; PID:g387122; GB:J03622; GB:
A:Note: the authors translated the codon TAT for residue 99 as Thr
R:Clayton, L.K.; Sayre, P.H.; Novotny, J.; Reinherz, E.L.

A;Status: not compared with conceptual translation

A; Cross-references: EMBL:X07871
 C; Comment: CD2 is a surface antigen expressed on all peripheral blood T-cells. It appears to be closely associated with, the erythrocyte receptor.

C:Generics:
A:Gene: GDB: CD2
A:Cross-References: GDB:118735; OMIM:186990
A:Map position: 1p13.1-1p13.1
A:Introns: 21/1; 128/1; 205/1; 246/1
C:Superfamily: T-cell surface glycoprotein CD2
C:Keywords: glycoprotein; T-cell; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-351/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
F:25-236/Domain: extracellular #status predicted <EXT>
F:210-234/Domain: transmembrane #status predicted <TM>
F:237-351/Domain: intracellular #status predicted <INT>
F:89,141,150/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	7.7%	Score 136.5;	DB 1;	Length 351;
Best Local Similarity	23.9%;	Pred. No. 0.0013;		
Matches	71;	Conservative 44;	Mismatches 111;	Indels 71; Gaps 15;
QY	28	ELVSGVGAVTFPLKS--KVKQVDSIW--TFNTPLEVTIQPEGGTIIVTQNRNRVDVF	83	
Db		:	:	:
Db	32	ETWALGQDINLDIPFSQMSDDIDDKWEKTSKKIAQFRKEKTF--KEKDIYKL-F	87	
QY	84	PDGGYSLKSLKNDSDGYLYVGIYSSSLQQPSTQBYVLHVYHLSPKPVWGLQSNKNG	143	
Db		:	:	:
Db	88	KNG--TLKIKHLKTTDQDDIYKSVIYDTGKNVLEKIFDLKIQERVSKPKISW-----	137	
QY	144	TCV-TNLTCMBEHEEDVYTWKALQQAANESHGSIPLISWR-----WGES-DMTFTICV	196	
Db		:	:	:
Db	138	TCINTTLTCEVNGTDPEL-----NLQDGKHLKLSQRVITHKWTLSAKFKCT	187	
QY	197	ARNPVSIRNFS-SPI-----LARKLCEGAADDPDSSMWLLCLLAVPLILLSLVLGL	245	
Db		:	:	:
Db	188	AGNKVSKSSSVFSPCEPKGLDIYLIIGCGGS-----LLMVFAALL	230	
QY	246	FLWFLLKRERQOEYIEBEKRVDICRTFNPICPHSGENTGYDTDIPHTNRITLKEDPANT	302	
Db		:	:	:
Db	231	VFYITKRKKQ-----RSRRNDDELETR---AHRVATEERGRKPHQIPASTPONPATS	279	

RESULT 6
SO1299
OX-45 membrane glycoprotein precursor - rat
N:Alternate names: MRC OX-45 antigen
C:Species: Rattus norvegicus (Norway rat)
E:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
F:Accession: SO1299
R:Killean, N.; Moessner, R.; Arvieux, J.; Willis, A.; Williams, A.F.
S:EMBL J. 7, 3087-3091, 1988
T:Title: The MRC OX-45 antigen of rat leukocytes and endothelium is in a subset of the i
U:Reference number: SO1299; MUID:89030603; PMID:3181129
V:Accession: SO1299
W:Molecule type: mRNA
X:Residues: 1-240 <KIL>
Y:Cross-references: EMBL:X13016; NID:G56804; PIDN:CAA31438.1; PID:G56805
Z:Superfamily: B-cell surface glycoprotein blast-1
Keywords: glycoprotein; membrane protein; surface antigen
1-22/Domain: signal sequence #status predicted <Sig>
23-240/Product: OX-45 membrane glycoprotein #status predicted <Mat>
38,97,140,186,203/Binding site: carbohydrate (Asn) (covalent) #status predicted

	Query Match	7.6%	Score 134;	DB 2;	Length 240;
	Best Local Similarity	24.6%;	Pred. No. 0.0013;		
	Matches 48;	Conservative 33;	Mismatches 104;	Indels 10;	Gaps 4;
13	ILWQLTGSAAAGPVKELVGSV----	CGAVTFP-LKSKVKQVDSIVVTFNTPLVTTQDEG	67		
			:		
11	ILESLLLSLVTFGQDQSVPNVAITG	SNVTLTLKHPILASVQRLTWLHTTNQKILEYFPN	70		
			:		
68	GTIIIVTQNRNRVDFPDGYSKLLKKNDSGIIYYVGVISLSSQQPSTQEXVLHVYEH	127			
			:		

Db 71 GKTVESVFKVDLDTKNGALRIYNSKEDRGYNNRMLHETDQ---WKITMEVYDL 127

Qy 128 LSPKVTMGLOSKNGKTCVTNLTCCMEHGEEDVYTWKALQAAANESHGNSILPISWRWG 187

Db 128 VSKPAIKIBKTNLTDSCHLRLSCKVE--DQGVDTWYEDSGPPFPNGVGLIETTPH 185

Qy 188 ESDMTFICVARNPVS 202

Db 186 NKSTFYTCQVSNPVS 200

RESULT 7
RWRTC2
T-cell surface glycoprotein CD2 precursor - rat
N:Alternate names: CD2 antigen; OX-34 antigen
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 25-Oct-1996
C:Accession: A33071; B27560; A27560; A32346
R:Barclay, A.N.; Williams, A.F.
submitted to the EMBL Data Library, May 1987
A:Reference number: A33071
A:Accession: A33071
A:Molecule type: mRNA
A:Residues: 1-344 <BAR>
R:Williams, A.F.; Barclay, A.N.; Clark, S.J.; Paterson, D.J.; Willis, A.C.
J. Exp. Med. 165, 368-380, 1987
A:Title: Similarities in sequences and cellular expression between rat CD2 and CD4 antigens
A:Reference number: A27560; MUID:87139793; PMID:3102667
A:Accession: B27560
A:Molecule type: protein
A:Residues: 'X', 24-52, 'X', 54-55, 'X', 57-62; 93-109; 119-150; 238-245 <WII>
A:Accession: A27560
A:Molecule type: mRNA
A:Residues: 44-344 <WII2>
A>Note: 112-Asn was also found
R:He, Q.; Beyers, A.D.; Barclay, A.N.; Williams, A.F.
Cell 54, 979-984, 1988
A:Title: A role in transmembrane signaling for the cytoplasmic domain of the CD2 T lymphocyte antigen
A:Reference number: A32346; MUID:88327862; PMID:2901293
A:Accession: A32346

Cross-references: GS:X05111
 C:Superfamily: T-cell surface glycoprotein CD2
 C:Keywords: glycoprotein; T-cell; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-34/Product: T-cell surface glycoprotein CD2 #status predicted <MAT>
 F:23-34/Domain: extracellular #status predicted <EXT>
 F:200-228/Domain: transmembrane #status predicted <TM>
 F:229-344/Domain: intracellular #status predicted <INT>
 F:199,106,134/Binding site: carbohydrate (Asn) #status experimental

Query Match	7.3%;	Score 130;	DB 1;	Length 344;
Best Local Similarity	22.4%;	Pred. No. 0.0044;		
Matches	65;	Conservative 51;	Mismatches 112;	Indels 62; Gaps 13;
2Y	12	YILWQLTGSAA-----SGPKVLGVSGGAVTFPLKSKVKQVDSIVTFTNTPLVTIQPEG	67	
2b	10	FLFSLSSKGACRDSGTWVGALGR-GINLNPINQMOTDDIDEVRW-----ER	56	
2Y	68	GTTIVTQNNRRERVPDPGGY-----SLKLSLKQNDSDGIYYVGIYSSSLQOPSTQEVV	121	
2b	57	GSTLVAEAFRRKMKPFLKSGAFEILANGDLKIKNLTRDSDGYNNVYVSTNGTRILDKALD	116	
2Y	122	LHWYEHLSKPKVTMGLQNKNGTCV---TNLTCCMEHGEDIYTWKALGOARANESHG	177	
2b	117	LRILEMVSKEPMIYWC-SNATLTCEVLEGTDVELKTYQGKEHL-----RSURQT-----	165	
2Y	178	SILPTISWRNGSDMTFICVARNVPSRNFSSPILARKICEGAADDPSSMVLCLLVLPL-	236	
2b	166	-----MSYQWNTLRAFPKCAVNRVSOSEMEV-----NCPEKGPLYLIIVGSAG	212	
Y	237	-LLSUFVLGLFWLFL-----KREROEYIEEK-KRVDICRETPNCPHS	278	

Db 183 TPQNKSTFYTCQVSNPVSCKNDTVYFTLPCLARSSGVCWTA-----TWLVVTTLIHRI 237

F;1-138/Domain: carcin

F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 A:Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476
 R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
 A:Reference number: A32164
 A:Contents: erratum
 A:Accession: A32164
 A:Molecule type: mRNA
 A:Residues: 1-526 <HIN>
 A:Cross-references: GB:J03858; NID:g179439; PIDN:AAA51826.1; PID:g179440
 R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
 A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of A:Reference number: A94206; MUID:88320555; PMID:2457922
 A:Contents: annotation
 A>Note: the sequence shown in this reference has been completely corrected in reference R:Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Eling, J.J.; K J. Cell Biol. 108, 267-276, 1989
 A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNA A:Reference number: A92752; MUID:89139550; PMID:2537311
 A:Accession: A30127
 A:Molecule type: mRNA
 A:Residues: 1-526 <BARI>
 A:Cross-references: EMBL:X16354; NID:g37197; PIDN:CAA34404.1; PID:g37198; EMBL:X14784
 A:Experimental source: splice form a
 A:Accession: B30127
 A:Molecule type: mRNA
 A:Residues: 1-319, 'D', 417-526 <BAR2>
 A:Cross-references: EMBL:X14831; NID:g37199; PIDN:CAA32940.1; PID:g37200; EMBL:X14784
 A:Experimental source: splice form b
 R:Barnett, T.R.; Drake, L.; Pickle II, W. Mol. Cell. Biol. 13, 1273-1282, 1993
 A:Title: Human biliary glycoprotein gene: characterization of a family of novel alternat A:Reference number: A48078; MUID:93140765; PMID:8423792
 A:Accession: A48078
 A:Molecule type: mRNA
 A:Residues: 124-141, 'H', 417-526 <BAR3>
 A:Cross-references: GB:M76742; NID:g179480; PIDN:AAA57142.1; PID:g179481
 A:Experimental source: splice form x
 A>Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:P:123606)
 R:Hauck, W.; Nedellec, P.; Turbide, C.; Stammers, C.P.; Barnett, T.R.; Beauchemin, N. Eur. J. Biochem. 223, 529-541, 1994
 A:Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene fami A:Reference number: S45664; MUID:94333343; PMID:8055923
 A:Accession: S45664
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-21 <HAU>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 R:Nedellec, P.; Turbide, C.; Beauchemin, N. Eur. J. Biochem. 231, 104-114, 1995
 A:Title: Characterization and transcriptional activity of the mouse biliary glycoprotein A:Reference number: S65939; MUID:95354678; PMID:7628460
 A:Accession: S65939
 A>Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-21 <NED>
 A:Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; PID:g606777
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
 A>Note: only a part of the coding sequence is given
 R:Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Hammarstrom, S. Genomics 14, 384-390, 1992
 A:Title: Identification of three new genes and estimation of the size of the carcinoemb A:Reference number: A44476; MUID:93052339; PMID:1427854
 A:Contents: annotation; alignment of related sequences
 C:Genetics:
 A:Gene: GDB:BGP
 A:Cross-references: GDB:127992; OMIM:109770
 A:Map position: 19q13.2-19q13.2
 C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin A:Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein
 P:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>
 F:35-428/Domain: extracellular #status predicted <EXT>
 F:35-319, 'D', 417-526/Product: biliary glycoprotein 1, splice form b #status predicted <F>
 F:35-141, 'H', 417-526/Product: biliary glycoprotein 1, splice form x #status predicted <F>
 F:160-217/Domain: immunoglobulin homology <IMM1>
 F:252-301/Domain: immunoglobulin homology <IMM2>
 F:341-398/Domain: immunoglobulin homology <IMM3>
 F:425-454/Domain: transmembrane #status predicted <TMM>
 F:453-526/Domain: intracellular #status predicted <INT>
 F:104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/B

Query Match 7.1%; Score 125.5; DB 1; Length 526;
 Best Local Similarity 25.1%; Pred. No. 0.017;
 Matches 67; Conservative 36; Mismatches 93; Indels 71; Gaps 17;

QY 68 GTIIIVTQ-----NRNRRVDFPDGGYSLKSLKLNDSGIYVIGYSSSL-QQPSIOE 119
 DB 81 GVAICTQATPGPANSGRHETI-YPNA--SLLIQNTQNDTGYTIQVILKSDLVNBEATCQ 137
 QY 120 YVLHVYHLSKPKVTMGLQSNKNGTCVTNLTCCMHGDEEDVIYTWKALGQAAANESHGSI 179
 DB 138 F--HYVPELPKPSISSNNSNPVEDKDAVATC--EPETQDTTYLAWI-----NNQS 184
 QY 180 LPISRW--GESDMTFCIVAR-----NPVRNFPSSPILARKLCBG-----A 218
 DB 185 LPVSPRLQLSNGNRTLTLLSVTRNDTPGYCEIQNPVSANRSDPV-TLNVTYGPDTPTIS 243
 QY 219 ADD----PDSSNVILCLLL--VPLLLSLFVLGLFLWFLKREOEYIEKKRVDICRETP 272
 DB 244 PSDTYRFGANLSUSCYAASNPAPQYSWLINGTF----QOSTQELFI-----P 287
 QY 273 NI-CPHSGENTHEY--DTIPHTNRTILK 296
 DB 288 NITVNSGYSYCHANNVSGCNRTTVK 314

RESULT 14
 A27681
 nonspecific cross-reacting antigen precursor - human
 N:Alternate names: NCA; TEX/NCA
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1989 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000
 A:Accession: A26902; A29875; A27681; B31037; A29918; A27709; A36271; C26414; E44476; F44
 R:Oikawa, S.; Kosaki, G.; Nakazato, H.
 Biochem. Biophys. Res. Commun. 146, 464-469, 1987
 A:Title: Molecular cloning of a gene for a member of carcinoembryonic antigen (CEA) gen A:Reference number: A26902; MUID:87298464; PMID:3619891
 A:Accession: A26902
 A:Molecule type: DNA
 A:Residues: 1-141 <OIK>
 A:Cross-references: GB:M17082; NID:g180230; PIDN:AAA51971.1; PID:g553222
 R:Thompson, J.A.; Pande, H.; Paxton, R.J.; Shively, L.; Padma, A.; Simmer, R.L.; Todd, Proc. Natl. Acad. Sci. U.S.A. 84, 2965-2969, 1987
 A:Title: Molecular cloning of a gene belonging to the carcinoembryonic antigen gene fam A:Reference number: A29875; MUID:87204248; PMID:3033672
 A:Accession: A29875
 A:Molecule type: DNA
 A:Residues: 23-141 <THO>
 A:Cross-references: GB:M16337
 A>Note: the authors translated the codon ACT for residue 64 as Tyr
 R:Tawaragi, Y.; Oikawa, S.; Matsuo, Y.; Kosaki, G.; Nakazato, H. Biochem. Biophys. Res. Commun. 150, 89-96, 1988
 A:Title: Primary structure of nonspecific crossreacting antigen (NCA), a member of carc A:Reference number: A27681; MUID:88106638; PMID:3337731
 A:Accession: A27681
 A:Molecule type: mRNA
 A:Residues: 1-238, 'V', 240-344 <TAW>
 A:Cross-references: GB:M18728; NID:g189084; PIDN:AAA59907.1; PID:g189085
 R:Barnett, T.; Goebel, S.J.; Notthdurft, M.A.; Eling, J.J. Genomics 3, 59-66, 1988
 A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and A:Reference number: A31037; MUID:89122014; PMID:3220478

A;Accession: B31037
A;Molecule type: mRNA
A;Residues: 1-137,'L',139-344 <BAR>
A;Cross-references: GB:M29541; NID:g189103; PIDN:AAA59915.1; PID:g189104
A;Note: the authors translated the codon TTG for residue 138 as Phe
R;Neumaier, M.; Zimmermann, W.; Shively, L.; Hinoda, Y.; Riggs, A.D.; Shively, J.E.
J. Biol. Chem. 263, 3202-3207, 1988
A;Title: Characterization of a cDNA clone for the nonspecific cross-reacting antigen (NC
A;Reference number: A29918; MUID:8819389; PMID:2830274
A;Accession: A29918
A;Molecule type: mRNA
A;Residues: 1-344 <NEU>
A;Cross-references: GB:M18216; GB:J03550; NID:g178690; PIDN:AAA51739.1; PID:g178691
R;Grubert, F.; Kolbinger, F.; Schwarz, K.; Schwaiblmair, H.; von Kleist, S.
Biochem. Biophys. Res. Commun. 153, 1105-1115, 1988
A;Title: Protein analysis of NCA-50 shows identity to NCA cDNA deduced sequences and ind
A;Reference number: A27709; MUID:8826882; PMID:3390172
A;Accession: A27709
A;Molecule type: protein
A;Residues: 35-95;99-120;123-138;149-151,'X',153-162;166,'X',174-193;231-235
R;Hefta, S.A.; Paxton, R.J.; Shively, J.E.
J. Biol. Chem. 265, 8618-8626, 1990
A;Title: Sequence and glycosylation site identity of two distinct glycoforms of nonspeci
A;Reference number: A36271; MUID:90256782; PMID:2341397
A;Accession: A36271
A;Molecule type: protein
A;Residues: 35-42;44-53;55-80;83-134;139-160;166-172;174-180;191-194,204-224;233-308;310
R;Paxton, R.J.; Mooser, G.; Pande, H.; Lee, T.D.; Shively, J.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 920-924, 1987
A;Title: Sequence analysis of carcinoembryonic antigen: identification of glycosylation
A;Reference number: A26414; MUID:87147209; PMID:3469650
A;Accession: C26414
A;Molecule type: protein
A;Residues: 35-69 <PAX>
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoemb
A;Reference number: A4476; MUID:93052339; PMID:1427854
A;Accession: E4476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KHA>
A;Accession: F44476
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-137,'L',139-141 <KH2>
C;Comment: This protein appears to be processed at the carboxyl terminus and anchored th
C;Genetics:
A;Gene: GDB:NCA
A;Cross-references: GDB:120221; OMIM:163980
A;Map position: 19q13.2-19q13.2
A;Introns: 22/1
A;Note: the list of introns may be incomplete
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termi
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphat
F;1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CRAN>
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-320/Product: nonspecific cross-reacting antigen #status experimental <MAT>
F;160-217/Domain: immunoglobulin homology <IMM1>
F;232-301/Domain: immunoglobulin homology <IMM2>
F;321-344/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;104,111,115,152,173,197,224,256,274,288,292/Binding site: carbohydrate (Asn) (covalent
F;309/Binding site: carbohydrate (asn) (covalent) #status predicted
F;320/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form

Query Match 7.0%; Score 124.5; DB 2; Length 344;
Best Local Similarity 22.4%; Pred. No. 0.012;
Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;
QY 53 WTENPLPLVTLTIQ-----PEGGTII-----VTQNR-----NRERVD----- 82.
Db 28 WNPFTAKLTLESTFPNVAEGREKVELLAHLNLPQNRIGYSWYGERVDGSLIVGYVIGTQ 87

Db 88 KTTGPAHSGRETVYNGSLIORVTKDTGVYTIEMTDENFRR--TEATVQFHVHQLLL 145
Qy 130 KPKVTMGLOSNKXGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSILPISWRWGES 189
Db 146 KPNITSNNSNPVEGDDSVSLTCDSDYTDPDNITYLNSRNGESLSE---GDRLLKS--EGNR 200
Qy 190 DMT-----FICVARNPVSRNFSSP 208
Db 201 TLTLNVTNRNDTGPYVCETRNPSVNRSDP 230

Search completed: August 18, 2004, 15:52:53
Job time : 21 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:45:27 ; Search time 14 Seconds
(without alignments)
1245.964 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSTPCLTIYILWLTGS.....PHSLTMDPTRLRFAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	354.5	20.0	654	1 LY9_MOUSE	Q01965 mus musculus
2	318	17.9	655	1 LY9_HUMAN	Q9h997 homo sapien
3	186	10.5	343	1 SLAM_MOUSE	Q9qum4 mus musculus
4	182.5	10.3	335	1 SLAM_HUMAN	Q13291 homo sapien
5	144	8.1	344	1 CD2_MOUSE	P08920 mus musculus
6	134	7.6	240	1 CD48_RAT	P10252 rattus norv
7	133.5	7.5	351	1 CD2_HUMAN	P06729 homo sapien
8	130	7.3	344	1 CD2_RAT	P08921 rattus norv
9	126.5	7.1	240	1 CD48_MOUSE	P18181 mus musculus
10	125.5	7.1	526	1 CE41_HUMAN	P13688 homo sapien
11	124.5	7.0	344	1 CE46_HUMAN	P40199 homo sapien
12	119.5	6.7	365	1 CXAR_HUMAN	P78310 homo sapien
13	116.5	6.6	319	1 A33_HUMAN	Q99795 homo sapien
14	114.5	6.5	702	1 CE45_HUMAN	P06731 homo sapien
15	113.5	6.4	521	1 CE41_MOUSE	P31809 mus musculus
16	110.5	6.2	463	1 CD4_CANFA	P33705 canis famil
17	105.5	6.0	329	1 CD86_HUMAN	P42081 homo sapien
18	102.5	5.8	519	1 ECTO_RAT	P16573 rattus norv
19	101	5.7	349	1 CEAB_HUMAN	P31997 homo sapien
20	101	5.7	349	1 LACH_SCHAM	Q26474 schistocerc
21	101	5.7	588	1 C166_CHICK	P42292 gallus gall
22	100.5	5.7	555	1 C166_CARAU	Q90304 carassius a
23	99	5.6	417	1 PVR_CERAE	P32506 cercopithec
24	98.5	5.6	526	1 BUTY_BOVIN	P18892 bos taurus
25	98	5.5	347	1 CD2_HORSE	P37998 equus cabal
26	98	5.5	503	1 SHS1_HUMAN	P78324 h protein-t
27	98	5.5	1382	1 MET_RAT	P97523 rattus norv
28	97	5.5	773	1 PIGR_RABIT	P01832 oryctolagus
29	96	5.4	359	1 LACH_DROME	Q24372 drosophila
30	96	5.4	526	1 BUTY_HUMAN	Q13410 homo sapien
31	96	5.4	1087	1 PGDS_XENLA	P26619 xenopus lae
32	96	5.4	1451	1 MYM1_HUMAN	P52179 homo sapien
33	95.5	5.4	365	1 CXAR_MOUSE	P97792 mus musculus

34	95.5	5.4	700	1 PTPE_HUMAN	P23469 homo sapien
35	95.5	5.4	771	1 PIGR_MOUSE	Q70570 mus musculus
36	95.5	5.4	822	1 CAN3_SHEEP	Q9tth8 ovis aries
37	94	5.3	233	1 GP42_RAT	P23505 rattus norv
38	94	5.3	1088	1 NCA1_XENLA	P16170 xenopus lae
39	93	5.2	419	1 PSG4_HUMAN	Q00888 homo sapien
40	93	5.2	419	1 PSG7_HUMAN	Q13046 homo sapien
41	93	5.2	535	1 PYRG_SPICI	P52200 spiroplasma
42	92.5	5.2	299	1 JAM1_HUMAN	Q9Y624 homo sapien
43	92.5	5.2	330	1 CD86_RABIT	P42071 oryctolagus
44	92.5	5.2	564	1 C166_BRARE	Q90460 brachydanio
45	91	5.1	491	1 KCS3_RABIT	Q9t17 oryctolagus
46	91	5.1	822	1 CAN3_BOVIN	P51186 bos taurus
47	91	5.1	1548	1 SMCY_MOUSE	Q62240 mus musculus
48	90.5	5.1	417	1 PVR_HUMAN	P15151 homo sapien
49	90.5	5.1	1905	1 Y655_PASMU	Q9cmz1 pasteurella
50	90	5.1	250	1 LPA3_HUMAN	P19256 homo sapien
51	90	5.1	419	1 PSG1_HUMAN	P11464 homo sapien
52	90	5.1	541	1 IRI8_HUMAN	Q13478 homo sapien
53	89.5	5.1	243	1 CD48_HUMAN	P09326 homo sapien
54	89.5	5.1	349	1 OMPA_BUCAL	P57414 buchnera ap
55	89.5	5.1	821	1 CAN3_PIG	P43368 sus scrofa
56	89.5	5.1	1051	1 YC94_HUMAN	Q9p2q2 homo sapien
57	89	5.0	309	1 CD86_MOUSE	P42082 mus musculus
58	89	5.0	821	1 CAN3_HUMAN	P20807 homo sapien
59	88.5	5.0	271	1 OX2V_KSHV	P88963 kaposi's sa
60	88.5	5.0	327	1 MOXR_RAT	Q9es58 rattus norv
61	88.5	5.0	1390	1 MET_HUMAN	P08581 homo sapien
62	88	5.0	363	1 MURG_BORBU	O51708 borrelia bu
63	88	5.0	508	1 CD5_DROME	Q9vfp1 drosophila
64	88	5.0	509	1 SHS1_RAT	P97710 r protein-t
65	88	5.0	530	1 PVR2_MOUSE	P32507 mus musculus
66	88	5.0	699	1 PTPE_MOUSE	P49446 mus musculus
67	88	5.0	821	1 CAN3_RAT	P16259 rattus norv
68	88	5.0	1092	1 NCA2_XENLA	P36335 xenopus lae
69	88	5.0	6669	1 NEBU_HUMAN	P20929 homo sapien
70	87.5	4.9	265	1 CE47_HUMAN	Q14002 homo sapien
71	87.5	4.9	422	1 K3L1_RAT	P83556 rattus norv
72	87.5	4.9	769	1 PIGR_RAT	P15083 rattus norv
73	87	4.9	457	1 CD4_MOUSE	P06332 mus musculus
74	87	4.9	491	1 KCS3_HUMAN	Q9bq31 homo sapien
75	87	4.9	583	1 C166_HUMAN	Q13740 homo sapien
76	87	4.9	1666	1 MYM1_MOUSE	Q62234 mus musculus
77	87	4.9	3707	1 PGBM_MOUSE	Q05793 mus musculus
78	86.5	4.9	443	1 KX7L_VIBVU	Q8df05 vibrio vuln
79	86	4.9	348	1 KIL0_RAT	Q92018 rattus norv
80	86	4.9	354	1 VGLI_VZVD	P05258 varicella-z
81	85.5	4.8	978	1 KPMS_FSVMD	P00545 feline sarc
82	85.5	4.8	2491	1 MPRI_HUMAN	P11717 homo sapien
83	85	4.8	402	1 RAGE_RAT	Q63495 rattus norv
84	85	4.8	428	1 PSG3_HUMAN	Q16557 homo sapien
85	85	4.8	821	1 CAN3_MOUSE	Q64691 mus musculus
86	84.5	4.8	292	1 Y152_HUMAN	Q14165 homo sapien
87	84.5	4.8	583	1 C166_MOUSE	Q64490 mus musculus
88	84.5	4.8	1211	1 M10L_HUMAN	Q6bxt6 homo sapien
89	84	4.7	668	1 PSB2_YEAST	P08018 saccharomyc
90	84	4.7	1300	1 IRR_MOUSE	Q9wt14 mus musculus
91	84	4.7	1379	1 MET_MOUSE	P16056 mus musculus
92	84	4.7	1379	1 CLRI_MOUSE	O35161 mus musculus
93	83.5	4.7	298	1 JAM2_HUMAN	P57087 homo sapien
94	83	4.7	463	1 STHA_PSEFL	O05139 pseudomonas
95	83	4.7	757	1 PIGR_BOVIN	P81265 bos taurus
96	83	4.7	873	1 LDVR_HUMAN	P98155 homo sapien
97	83	4.7	1106	1 ACLY_CAEEL	P53585 caenorhabdi
98	82.5	4.7	773	1 MES2_CAEEL	O17514 caenorhabdi
99	82	4.6	386	1 NATB_BACSU	P46904 bacillus eu
100	82	4.6	609	1 HEMA_RINDR	P41355 rinderpest
101	82	4.6	880	1 TYO3_MOUSE	P55144 mus musculus
102	82	4.6	1007	1 GRD2_HUMAN	Q43424 homo sapien
103	82	4.6	3562	1 PGCV_CHICK	Q90953 gallus gall
104	81.5	4.6	278	1 OX2G_RAT	P04218 rattus norv
105	81.5	4.6	302	1 ICOL_HUMAN	O75144 homo sapien
106	81.5	4.6	378	1 LEUK_RAT	P13838 rattus norv

107	81.5	4.6	497	1	GALT_CLOAB	Q97ez4	clostridium	180	77	4.3	894	1	MTP_MOUSE	O08601	mus musculus
108	81.5	4.6	709	1	Y939_SULTO	Q97g3	sulfolobus	181	77	4.3	1041	1	EGT2_YEAST	P42835	saccharomyc
109	81.5	4.6	815	1	CAN3_NACFA	Q9glg7	macaca fasc	182	77	4.3	1448	1	PK3G_HUMAN	O57547	homo sapien
110	81.5	4.6	925	1	W70T_HUMAN	P57737	homo sapien	183	77	4.3	1897	1	PTPF_HUMAN	P10586	homo sapien
111	81	4.6	338	1	LAMP_HUMAN	Q13449	homo sapien	184	77	4.3	4870	1	YR3_HUMAN	Q9v0d0	pyrococcus
112	81	4.6	489	1	C302_DROME	Q9hgk9	drosophila	185	76.5	4.3	191	1	MOBA_PYRAB	Q08887	homo sapien
113	81	4.6	760	1	YCB5_YEAST	P22574	saccharomyc	186	76.5	4.3	426	1	PSG9_HUMAN	Q08340	macaca name
114	81	4.6	829	1	CAD3_HUMAN	P22223	homo sapien	187	76.5	4.3	458	1	CD4_MACNE	Q08340	macaca name
115	81	4.6	1304	1	NRCA_HUMAN	Q92823	homo sapien	188	76.5	4.3	497	1	UBID_ECOLI	P26615	escherichia
116	81	4.6	1341	1	UBR1_KLULA	O60014	kluyveromyc	189	76.5	4.3	1071	1	SEF1_KLULA	P87164	kluyveromyc
117	80.5	4.5	346	1	EPB1_HUMAN	P98172	homo sapien	190	76.5	4.3	1089	1	PGDS_HUMAN	P16234	homo sapien
118	80.5	4.5	462	1	MURD_CLOAB	Q97eb9	clostridium	191	76.5	4.3	1124	1	TCF8_HUMAN	P37275	homo sapien
119	80.5	4.5	476	1	YCAM_ECOLI	P75835	escherichia	192	76.5	4.3	1156	1	NI33_HUMAN	Q8wum0	homo sapien
120	80.5	4.5	1364	1	BLM_XENLA	Q9dey9	xenopus lae	193	76.5	4.3	1328	1	HUS2_SCHPO	Q09811	schizosacch
121	80.5	4.5	1948	1	PTNS_HUMAN	Q13332	homo sapien	194	76.5	4.3	1802	1	HKR1_YEAST	P41809	saccharomyc
122	80.5	4.5	3343	1	YOG7_CAEEL	P34616	caenorhabdi	195	76	4.3	138	1	PSAD_FREDI	P33808	fremyella d
123	80.5	4.5	3354	1	CAD7_MOUSE	Q99pf4	mus musculus	196	76	4.3	262	1	YCVI_ECOLI	P51983	escherichia
124	80.5	4.5	3358	1	PGCV_MOUSE	Q62059	mus musculus	197	76	4.3	316	1	DDL_ENTGA	Q47823	enterococc
125	80.5	4.5	6632	1	UNB9_CAEEL	O01761	caenorhabdi	198	76	4.3	333	1	AMAL_DROME	P15364	drosophila
126	80	4.5	338	1	LAMP_RAT	Q62813	rattus norv	199	76	4.3	417	1	PGCB_FELCA	P41725	felis silve
127	80	4.5	341	1	K2L3_HUMAN	P43628	h.killer ce	200	76	4.3	487	1	DPD2_YEAST	P46957	saccharomyc
128	80	4.5	482	1	ARCD_PSEAE	P18275	pseudomonas	201	76	4.3	524	1	BUTY_MOUSE	Q82556	mus musculus
129	80	4.5	1040	1	AXOI_HUMAN	Q02246	homo sapien	202	76	4.3	977	1	KFMS_MOUSE	P09581	mus musculus
130	80	4.5	1170	1	TSP1_MOUSE	P35441	mus musculus	203	76	4.3	978	1	KFMS_RAT	Q00495	rattus norv
131	79.5	4.5	249	1	MYPO_CHICK	P37301	gallus gall	204	76	4.3	2029	1	LAR_DROME	P16621	drosophila
132	79.5	4.5	328	1	TPSN_CHICK	P25251	braessica na	205	75.5	4.3	246	1	MOG_BOVIN	P55803	bos taurus
133	79.5	4.5	430	1	TPSN_CHICK	O73895	gallus gall	206	75.5	4.3	321	1	TCB_FLV	P11364	feline leuk
134	79.5	4.5	490	1	TIME_ECOLI	Q47282	escherichia	207	75.5	4.3	421	1	MPRI_SCHPO	O94423	schizosacch
135	79.5	4.5	740	1	PEC1_PIG	Q95242	sus scrofa	208	75.5	4.3	446	1	EX7L_STAPN	Q97qj8	streptococc
136	79.5	4.5	859	1	PMS2_MOUSE	P54279	mus musculus	209	75.5	4.3	458	1	CD4_MACFA	P79185	macaca fasc
137	79.5	4.5	873	1	LDVR_MOUSE	P98156	mus musculus	210	75.5	4.3	462	1	ALB3_ARATH	Q81bm4	arabidops
138	79.5	4.5	980	1	KFMS_FELCA	P13369	felis silve	211	75.5	4.3	498	1	MOO2_STAAM	Q8bm4	staphylococ
139	79.5	4.5	1465	1	MYM2_HUMAN	P54296	homo sapien	212	75.5	4.3	699	1	UVRG_HUMAN	Q9p2v5	homo sapien
140	79	4.5	438	1	Y232_METUA	Q60289	methanococc	213	75.5	4.3	1020	1	CONT_MOUSE	P12960	mus musculus
141	79	4.5	463	1	SHA_PSEPK	Q88ky8	pseudomonas	214	75.5	4.3	1089	1	PGDS_MOUSE	P28618	mus musculus
142	79	4.5	1228	1	ALU5_ARATH	Q98gg3	arabidopsis	215	75.5	4.3	2109	1	PGCA_CHICK	P07898	gallus gall
143	79	4.5	1361	1	GLI4_XENLA	Q91661	xenopus lae	216	75.5	4.3	3317	1	CADN_RAT	P58365	rattus norv
144	78.5	4.4	429	1	EPC_RAT	P01855	rattus norv	217	75	4.2	208	1	TRPF_CHLTR	O84331	chlamydia t
145	78.5	4.4	467	1	SIL5_MOUSE	Q91v57	mus musculus	218	75	4.2	239	1	CD8A_CANFA	P33706	canis famil
146	78.5	4.4	497	1	UBID_ECO57	P58194	escherichia	219	75	4.2	323	1	YAMB_THETU	P38541	thermoanaer
147	78.5	4.4	628	1	LU_HUMAN	P50895	homo sapien	220	75	4.2	332	1	CIB3_CAVPO	Q9qz20	cavia porce
148	78.5	4.4	831	1	SA53_YEAST	P34218	saccharomyc	221	75	4.2	543	1	EAAL_MOUSE	P56564	mus musculus
149	78.5	4.4	847	1	CD22_HUMAN	P20273	homo sapien	222	75	4.2	543	1	EAAL_MOUSE	P24942	rattus norv
150	78.5	4.4	927	1	CDGD_HUMAN	Q9v5g3	homo sapien	223	75	4.2	641	1	CAN6_MOUSE	O35646	mus musculus
151	78.5	4.4	1036	1	AXOI_CHICK	P28685	gallus gall	224	75	4.2	641	1	CAN6_MOUSE	O35646	mus musculus
152	78	4.4	335	1	PSG5_HUMAN	Q15238	homo sapien	225	75	4.2	685	1	ENAP_STRPU	O88501	rattus norv
153	78	4.4	353	1	CEPU_CHICK	Q90773	gallus gall	226	75	4.2	703	1	LAGD_LACLA	P26613	strongyloce
154	78	4.4	609	1	HENA_RINDK	P12567	rinderpest	227	75	4.2	747	1	PHUA_ECOLI	P59852	lactococcus
155	78	4.4	761	1	NCA2_HUMAN	P13592	homo sapien	228	75	4.2	1091	1	NCA1_CHICK	P06971	escherichia
156	78	4.4	771	1	SM1A_DROME	Q24322	drosophila	229	75	4.2	1099	1	NRX1_HUMAN	O60721	homo sapien
157	78	4.4	848	1	NCA1_HUMAN	P13591	homo sapien	230	75	4.2	1256	1	NRCA_MOUSE	O810u4	mus musculus
158	78	4.4	884	1	CADB_XENLA	P33152	xenopus lae	231	75	4.2	1492	1	AT7A_RAT	P70705	rattus norv
159	78	4.4	993	1	DSG3_MOUSE	O35902	mus musculus	232	75	4.2	3396	1	PGCV_HUMAN	P13611	homo sapien
160	77.5	4.4	236	1	YULI_SCHPO	O74414	schizosacch	233	74.5	4.2	146	1	RMP3_CAVPO	Q8r4c4	cavia porce
161	77.5	4.4	239	1	CD8A_FELCA	P41688	felis silve	234	74.5	4.2	219	1	FLA4_PYRKO	Q9v2w8	pyrococcus
162	77.5	4.4	333	1	CIB1_CAVPO	Q9qz22	cavia porce	235	74.5	4.2	232	1	OVAX_CHICK	P01013	gallus gall
163	77.5	4.4	448	1	EX7L_STRR6	Q8dp9	streptococc	236	74.5	4.2	328	1	PDXA_VIBVU	O8ed3	vibrio vuln
164	77.5	4.4	490	1	CNA8_MOUSE	O8bj63	mus musculus	237	74.5	4.2	379	1	NLPD_ECOLI	P33648	escherichia
165	77.5	4.4	491	1	SVT9_HUMAN	Q86s6	homo sapien	238	74.5	4.2	544	1	YES_XIPHE	P27447	xiphophorus
166	77.5	4.4	510	1	MOQ_WIGBR	Q8dlv2	wiggleswort	239	74.5	4.2	688	1	RCQI_MOUSE	Q32129	mus musculus
167	77.5	4.4	513	1	SHS1_MOUSE	P97797	m.protein-t	240	74.5	4.2	688	1	LIP_STAEP	Q02510	staphylococ
168	77.5	4.4	650	1	LIB1_HUMAN	Q8nh16	h.leukocyte	241	74.5	4.2	741	1	YBIO_ECOLI	P75783	escherichia
169	77.5	4.4	739	1	VCA1_HUMAN	P19320	homo sapien	242	74.5	4.2	764	1	ICCR_DROME	O08180	drosophila
170	77.5	4.4	757	1	DNM1_YEAST	P54861	saccharomyc	243	74.5	4.2	881	1	ENV_SIVVK	P05884	simian immu
171	77.5	4.4	1912	1	PTPD_HUMAN	P23468	homo sapien	244	74.5	4.2	1007	1	GRD2_MOUSE	Q16225	mus musculus
172	77.5	4.4	1950	1	UBR1_YEAST	P19812	saccharomyc	245	74.5	4.2	1007	1	GRD2_RAT	Q32226	rattus norv
173	77	4.3	138	1	PSAD_NOSS8	P56596	nostoc sp.	246	74.5	4.2	1178	1	RPOB_MYCLE	Q30760	mycobacteri
174	77	4.3	278	1	OX2G_MOUSE	O54901	mus musculus	247	74.5	4.2	1522	1	BAI3_HUMAN	O60242	homo sapien
175	77	4.3	338	1	LAMP_CHICK	Q98919	gallus gall	248	74.5	4.2	1723	1	LY75_MOUSE	Q60767	mus musculus
176	77	4.3	491	1	KCS3_RAT	O88759	rattus norv	249	74.5	4.2	2012	1	DSCA_HUMAN	O60469	homo sapien
177	77	4.3	502	1	SKS1_YEAST	Q12505	saccharomyc	250	74.5	4.2	2459	1	MAPB_RAT	P15205	rattus norv
178	77	4.3	523	1	CP78_SOYEN	O48927	glycine max	251	74.5	4.2	4655	1	LRP2_HUMAN	P98164	homo sapien
179	77	4.3	873	1	LDVR_RABIT	P35953	cryptotolagus	252	74	4.2	148	1	LRP1_HUMAN	O60894	homo sapien

253	74	4.2	227	1	GPWA_CHLVCV	Q821n6 chlamydomphi	326	72	4.1	463	1	STHA_PSESM	Q884i6 pseudomonas
254	74	4.2	333	1	GCB_RAT	P20761 rattus norv	327	72	4.1	469	1	GABP_BACSU	P46349 bacillus su
255	74	4.2	384	1	NRFF_HAEIN	P44962 haemophilus	328	72	4.1	510	1	PUSH_ARATH	Q23928 arabidopsis
256	74	4.2	403	1	CD33_MOUSE	P63994 mus musculus	329	72	4.1	517	1	PVR1_HUMAN	Q15223 homo sapien
257	74	4.2	469	1	EC33_YEAST	P38248 saccharomyc	330	72	4.1	548	1	SEAS_TOBAC	Q40577 nicotiana t
258	74	4.2	645	1	SKB1_SCHPO	P78963 schizosacch	331	72	4.1	585	1	YHD9_YEAST	P38732 saccharomyc
259	74	4.2	687	1	TGM2_HUMAN	P21980 homo sapien	332	72	4.1	643	1	CD93_RAT	Q96t61 rattus norv
260	74	4.2	821	1	FGR2_MOUSE	P21803 mus musculus	333	72	4.1	646	1	MU18_HUMAN	Q4121 homo sapien
261	74	4.2	862	1	CD22_MOUSE	P35329 mus musculus	334	72	4.1	670	1	S213_HUMAN	P46721 homo sapien
262	74	4.2	862	1	SM4D_HUMAN	Q92854 homo sapien	335	72	4.1	776	1	AD28_MACFA	Q9xal6 macaca fasc
263	74	4.2	910	1	RD12_ARATH	Q8w3k3 arabidopsis	336	72	4.1	778	1	GCB_SAISC	Q46567 salmirel sci
264	74	4.2	1063	1	CZCA_ALCEU	P13511 alcaligenes	337	72	4.1	840	1	HS74_HUMAN	P34932 homo sapien
265	74	4.2	1063	1	CZCA_ALCEU	P94177 alcaligenes	338	72	4.1	840	1	ORC1_MOUSE	Q92in2 mus musculus
266	74	4.2	1165	1	CHS3_YEAST	P29465 saccharomyc	339	72	4.1	868	1	VRG2_RAT	Q35569 rattus norv
267	74	4.2	1561	1	Y34F_DROME	Q9w5d0 drosophila	340	72	4.1	901	1	VP3_BTW10	P12435 bluetongue
268	74	4.2	1709	1	SN_HUMAN	Q9b222 homo sapien	341	72	4.1	901	1	VP3_BTW11	Q65749 bluetongue
269	74	4.2	4344	1	DYHC_EMENI	P45444 emericella	342	72	4.1	901	1	VP3_BTW12	P55582 bluetongue
270	74	4.2	5217	1	HTSI_COCCA	Q01886 escherichia	343	72	4.1	901	1	VP3_BTW2A	Q65748 bluetongue
271	74	4.2	6781	1	RIAB_PEDV7	Q91av2 p replicase	344	72	4.1	1159	1	SOR2_HUMAN	Q969q0 homo sapien
272	73.5	4.1	321	1	YOR4_ADEG1	P20746 avian adeno	345	72	4.1	1186	1	SYLC_CABEL	Q09996 caenorhabdi
273	73.5	4.1	364	1	CD33_HUMAN	P20138 homo sapien	346	72	4.1	1348	1	VGR2_COTJA	P52583 coturnix co
274	73.5	4.1	428	1	PYRC_BACHD	Q9k9v7 bacillus ha	347	72	4.1	1306	1	KMLS_CHICK	P11799 gallus gall
275	73.5	4.1	458	1	CD4_MACFU	P79184 macaca fusc	348	72	4.1	2358	1	YEBJ_ECOLI	P76347 escherichia
276	73.5	4.1	458	1	CD4_MACFU	P16003 macaca mufa	349	71.5	4.0	229	1	VV_PI4HA	P21739 human para
277	73.5	4.1	695	1	VTXB_SYNVE	Q98993 synanceia v	350	71.5	4.0	291	1	HTPX_BUCBP	P59559 buchnera ap
278	73.5	4.1	850	1	NRG2_HUMAN	O14511 homo sapien	351	71.5	4.0	299	1	YJG8_YEAST	P40363 saccharomyc
279	73.5	4.1	873	1	LDVR_RAT	P98166 rattus norv	352	71.5	4.0	312	1	YC90_METUA	Q58686 methanococ
280	73.5	4.1	880	1	ENV_SIVML	P11267 simian immu	353	71.5	4.0	338	1	RTCA_METUA	Q60335 methanococ
281	73.5	4.1	1057	1	SEPI_YEAST	P34228 saccharomyc	354	71.5	4.0	339	1	MDH_METFE	P16142 methanother
282	73.5	4.1	1166	1	L2GL_DROPS	Q08470 drosophila	355	71.5	4.0	403	1	RAGE_MOUSE	Q62151 mus musculus
283	73.5	4.1	2301	1	POLG_TMEVD	P13899 t genome po	356	71.5	4.0	496	1	C71F_ARATH	P58046 arabidopsis
284	73.5	4.1	4544	1	LRPI_HUMAN	Q07954 homo sapien	357	71.5	4.0	498	1	MOO2_STAMH	P959230 staphylococ
285	73	4.1	175	1	RMP2_HUMAN	O60895 homo sapien	358	71.5	4.0	500	1	RT03_PROWI	P46740 prototheca
286	73	4.1	304	1	K2S2_HUMAN	P43631 homo sapien	359	71.5	4.0	515	1	GM11_METAC	Q8tmie6 methanosarc
287	73	4.1	322	1	Y268_BACHD	Q9k706 bacillus ha	360	71.5	4.0	526	1	SRC_RSVSR	P00524 rous sarcom
288	73	4.1	413	1	HEMO_HYACE	P25033 hyalophora	361	71.5	4.0	527	1	MM19_MOUSE	Q9Jni10 mus musculus
289	73	4.1	518	1	TT8_ARATH	Q9ft81 arabidopsis	362	71.5	4.0	537	1	PYRG_CHLVC	Q822t2 chlamydomphi
290	73	4.1	543	1	EAAL_AMBTI	O57321 ambystoma t	363	71.5	4.0	733	1	ERG7_RAT	P48450 rattus norv
291	73	4.1	576	1	ILIR_RAT	Q02955 rattus norv	364	71.5	4.0	764	1	PIGR_HUMAN	P401833 homo sapien
292	73	4.1	666	1	NOD_DROME	P18105 drosophila	365	71.5	4.0	919	1	HEX_ADEL2	P19900 human adeno
293	73	4.1	853	1	NCAL_BOVIN	P31836 bos taurus	366	71.5	4.0	923	1	ODOI_BUCAP	Q8k9n3 buchnera ap
294	73	4.1	853	1	PBPA_HAEIN	P31776 h penicilli	367	71.5	4.0	1032	1	I895_HAEIN	Q57124 haemophilus
295	73	4.1	901	1	VP3_BTW13	Q65750 bluetongue	368	71.5	4.0	1374	1	YQ3D_SCHPO	Q93984 schizosacch
296	73	4.1	901	1	VP3_BTW17	P03539 bluetongue	369	71.5	4.0	1377	1	RPOC_BORBU	O51349 borrelia bu
297	73	4.1	1072	1	ICF1_CHICK	P26007 gallus gall	370	71.5	4.0	1693	1	SAS_DROME	Q04164 drosophila
298	73	4.1	1515	1	YCET_YEAST	P39109 saccharomyc	371	71.5	4.0	2126	1	PXDE_MOUSE	Q920t6 mus musculus
299	73	4.1	3788	1	LYST_MOUSE	P97412 mus musculus	372	71.5	4.0	2468	1	MAPB_HUMAN	P46821 homo sapien
300	72.5	4.1	399	1	YGV7_SCHPO	O43021 schizosacch	373	71.5	4.0	3063	1	CA1C_HUMAN	Q99715 homo sapien
301	72.5	4.1	424	1	PSG6_HUMAN	Q15235 homo sapien	374	71	4.0	258	1	Y256_MYCPN	P75421 mycoplasma
302	72.5	4.1	435	1	PSG6_HUMAN	Q00889 homo sapien	375	71	4.0	334	1	EFB1_CHICK	O73612 gallus gall
303	72.5	4.1	440	1	YMT6_YEAST	Q04215 saccharomyc	376	71	4.0	343	1	G3P_SULTO	Q971k2 sulfolobus
304	72.5	4.1	443	1	TOLB_BRUME	Q93t54 brucella me	377	71	4.0	344	1	NTRI_MOUSE	Q99p10 mus musculus
305	72.5	4.1	443	1	TOLB_BRUME	Q8fz07 brucella su	378	71	4.0	344	1	NTRI_MOUSE	Q62718 rattus norv
306	72.5	4.1	485	1	DLTA_STAEP	Q8cc93 staphylococ	379	71	4.0	345	1	EFB1_MOUSE	P52795 mus musculus
307	72.5	4.1	657	1	MM15_MOUSE	O54732 mus musculus	380	71	4.0	389	1	CVB_DICDI	Q37311 dictyosteli
308	72.5	4.1	666	1	SLV1_YEAST	P22213 saccharomyc	381	71	4.0	417	1	GATD_PYRAE	Q82y04 pyrobaculum
309	72.5	4.1	686	1	IPL2_MOUSE	Q9ers6 mus musculus	382	71	4.0	455	1	YML8_YEAST	P43297 arabidopsis
310	72.5	4.1	851	1	NCL1_CABEL	P34511 caenorhabdi	383	71	4.0	462	1	RD21_ARATH	P43297 arabidopsis
311	72.5	4.1	867	1	ENV_HVIJ3	P12489 human immu	384	71	4.0	509	1	VMT9_MXVIL	P08073 myxoma viru
312	72.5	4.1	895	1	SECA_CYACA	O19911 cyanidium c	385	71	4.0	522	1	Y18J_SCHPO	Q9utal1 schizosacch
313	72.5	4.1	909	1	DDRI_PANTR	Q7yr43 pan troglod	386	71	4.0	551	1	HAS2_XENLA	O57427 xenopus lae
314	72.5	4.1	913	1	DDRI_HUMAN	Q08345 h epithelia	387	71	4.0	605	1	COG6_HUMAN	P9Y2v7 homo sapien
315	72.5	4.1	1013	1	SCA4_RICRH	Q9aj81 rickettsia	388	71	4.0	690	1	LIP_STAUA	P10335 staphylococ
316	72.5	4.1	1021	1	CONT_RAT	Q63198 rattus norv	389	71	4.0	690	1	LIP_STAUA	Q8ayc2 staphylococ
317	72.5	4.1	1165	1	LEPN_PIG	O02671 sus scrofa	390	71	4.0	727	1	PEC1_MOUSE	Q08481 mus musculus
318	72.5	4.1	1214	1	NRCA_RAT	P97686 rattus norv	391	71	4.0	821	1	FGR2_HUMAN	P21802 homo sapien
319	72.5	4.1	1369	1	NFAS_CHICK	O42414 gallus gall	392	71	4.0	905	1	XPF_HUMAN	Q92889 homo sapien
320	72.5	4.1	1434	1	PTCI_MOUSE	Q61115 mus musculus	393	71	4.0	922	1	W70T_MOUSE	Q942v7 mus musculus
321	72.5	4.1	2333	1	PGCA_CANFA	Q28343 canis famil	394	71	4.0	956	1	SVI_AQUAE	Q66551 aquifex aeo
322	72.5	4.1	2896	1	NSD1_HUMAN	Q96173 homo sapien	395	71	4.0	1018	1	CONT_HUMAN	Q12860 homo sapien
323	72.5	4.1	4367	1	DYHC_NEUCR	P45443 neurospora	396	71	4.0	1082	1	RGR1_YEAST	P19263 saccharomyc
324	72	4.1	384	1	Z183_CABEL	O17917 caenorhabdi	397	71	4.0	1240	1	YQ03_CABEL	Q09550 caenorhabdi
325	72	4.1	394	1	Z193_HUMAN	O15535 homo sapien	398	71	4.0	1338	1	VGR1_HUMAN	P17948 h vascular

399	71	4.0	4391	1	PGBM_HUMAN	P8160	homo sapien	472	69.5	3.9	346	1	NRL3_ARATH	P46010	arabidopsis
400	70.5	4.0	203	1	FLAI_ARCFU	O9208	archaeoglob	473	69.5	3.9	429	1	ARSB_STAEP	O8qf4	staphylococ
401	70.5	4.0	311	1	HTX1_SULTO	Q9732	sulfolobus	474	69.5	3.9	437	1	PUR8_AQUAE	O6856	aquifex aeo
402	70.5	4.0	332	1	PDXA_VIBPA	Q8785	vibrio para	475	69.5	3.9	444	1	TOUB_RICCN	Q9x114	rickettsia
403	70.5	4.0	333	1	MDHC_HUMAN	P40925	homo sapien	476	69.5	3.9	497	1	ANSP_SALTY	P40812	salmonella
404	70.5	4.0	338	1	MDHM_HUMAN	P40926	homo sapien	477	69.5	3.9	503	1	WSC2_YEAST	P53832	saccharomyc
405	70.5	4.0	338	1	MDHM_RAT	P04636	rattus norv	478	69.5	3.9	523	1	SRC_RSVPA	P31693	rous sarcom
406	70.5	4.0	429	1	ARSB_STAEP	Q91255	staphylococ	479	69.5	3.9	535	1	SRC_RAT	Q9wud9	rattus norv
407	70.5	4.0	455	1	K3L2_HUMAN	P43630	homo sapien	480	69.5	3.9	548	1	AMDS_EMENT	P08158	emericeella
408	70.5	4.0	526	1	SRC_AVISR	P00525	avian sarco	481	69.5	3.9	548	1	TPH1_HUMAN	P32780	homo sapien
409	70.5	4.0	532	1	SRC_CHICK	P00523	gallus gall	482	69.5	3.9	568	1	ULP1_SCHPO	O42957	schizosacch
410	70.5	4.0	537	1	YES_XENLA	P10936	xenopus lae	483	69.5	3.9	585	1	KNC1_RAT	P25122	rattus norv
411	70.5	4.0	545	1	PCR_FSVGR	P00544	feline sarc	484	69.5	3.9	616	1	Y396_HELPY	O25157	helicobacte
412	70.5	4.0	547	1	TPH1_MOUSE	Q9db89	mus musculus	485	69.5	3.9	633	1	AGP1_YEAST	P25376	saccharomyc
413	70.5	4.0	557	1	SRC_AVISR	P14085	avian sarco	486	69.5	3.9	682	1	PRC_ECOLI	P23865	escherichia
414	70.5	4.0	558	1	VP10_RBSDV	P19898	rice black	487	69.5	3.9	718	1	COAT_MUMIM	P07302	murine minu
415	70.5	4.0	568	1	SRC_AVISS	P25805	plasmodium	488	69.5	3.9	736	1	ME27_SCHPO	O94713	schizosacch
416	70.5	4.0	569	1	CYSP_PLAFA	P15054	avian sarco	489	69.5	3.9	751	1	FOH1_PIG	P07564	s glutamate
417	70.5	4.0	587	1	SRC_AVIS2	P14084	avian sarco	490	69.5	3.9	776	1	POLG_LANVY	P27454	aedes denso
418	70.5	4.0	610	1	CALG_HUMAN	O14967	homo sapien	491	69.5	3.9	849	1	VNCS_AEDRV	P27838	langat viru
419	70.5	4.0	627	1	MUTL_BACSU	P49850	bacillus su	492	69.5	3.9	1033	1	CIS1_MOUSE	P27454	aedes denso
420	70.5	4.0	630	1	MUC1_MOUSE	Q02496	mus musculus	493	69.5	3.9	1062	1	NAL2_HUMAN	Q84b8	mus musculu
421	70.5	4.0	641	1	CAN6_HUMAN	Q9y6q1	homo sapien	494	69.5	3.9	1178	1	RPOB_MYCTU	Q9nx02	homo sapien
422	70.5	4.0	648	1	GYRB_MYCGA	P47720	mycoplasma	495	69.5	3.9	1260	1	CAML_MOUSE	P47766	mycobacteri
423	70.5	4.0	686	1	IPL2_HUMAN	Q9np60	h x-linked	496	69.5	3.9	1604	1	UB32_HUMAN	P11627	mus musculu
424	70.5	4.0	787	1	OBP_HSV7J	P52379	human herpe	497	69.5	3.9	1722	1	LY75_HUMAN	Q8nfao	homo sapien
425	70.5	4.0	793	1	YEA8_SCHPO	O14073	schizosacch	498	69.5	3.9	3414	1	POLG_LANVY	O60449	homo sapien
426	70.5	4.0	843	1	EF2_DROME	P13060	drosophila	499	69	3.9	139	1	PSAD_ANASP	P29837	l genome po
427	70.5	4.0	877	1	CAD2_BOVIN	P19534	bos taurus	500	69	3.9	217	1	ALGF_PSRFL	P58573	anabaena sp
428	70.5	4.0	895	1	MTP_MESAU	P55158	mesocricetu	501	69	3.9	327	1	LI2B_MARMO	P29791	pseudomonas
429	70.5	4.0	906	1	CAD2_MOUSE	P15116	mus musculus	502	69	3.9	344	1	NTRI_HUMAN	Q61729	marmota mon
430	70.5	4.0	906	1	CAD2_RAT	Q9zly3	rattus norv	503	69	3.9	357	1	YOJ1_CABEL	Q9p121	homo sapien
431	70.5	4.0	928	1	PM15_CHLPN	Q9rb65	chlamydia p	504	69	3.9	390	1	Y109_NPVAC	P34624	caenorhabdi
432	70.5	4.0	938	1	PM15_CHLPN	Q92883	chlamydia p	505	69	3.9	394	1	ID12_PYRFU	P41662	autographa
433	70.5	4.0	984	1	SENT_HUMAN	Q9bqf6	homo sapien	506	69	3.9	458	1	PRTC_RABIT	Q8u2h9	pyrococcus
434	70.5	4.0	1200	1	HYAL_STRPU	O76536	strongyloce	507	69	3.9	490	1	CPC7_RAT	O28661	oryctolagus
435	70.5	4.0	1356	1	VGR2_HUMAN	P35968	homo sapien	508	69	3.9	497	1	VLI_BPV2	P05179	rattus norv
436	70.5	4.0	1454	1	CPSA_CABEL	Q9n4c2	caenorhabdi	509	69	3.9	505	1	ATPA_SYNP6	P06458	bovine papi
437	70.5	4.0	1694	1	SN_MOUSE	O62230	mus musculus	510	69	3.9	506	1	SHS1_BOVIN	P08449	synchococcc
438	70.5	4.0	2298	1	CU05_HUMAN	Q9z3r5	homo sapien	511	69	3.9	515	1	PVR1_PIG	O46631	bos taurus
439	70.5	4.0	2303	1	POLG_TWEVG	P08545	t genome po	512	69	3.9	523	1	C756_CAMME	Q9g176	sus scrofa
440	70.5	4.0	2454	1	MAPB_MOUSE	P14873	mus musculus	513	69	3.9	537	1	IR18_MOUSE	O40773	campanula m
441	70.5	4.0	2738	1	PGCV_RAT	Q9erb4	rattus norv	514	69	3.9	542	1	EAAL_HUMAN	O61098	mus musculus
442	70	4.0	115	1	KV5F_MOUSE	P01638	mus musculus	515	69	3.9	557	1	LLVD_BACAA	P43003	homo sapien
443	70	4.0	224	1	CM35_HUMAN	Q08708	homo sapien	516	69	3.9	584	1	NA6S_YEAST	Q81826	bacillus an
444	70	4.0	262	1	RPC_BPI63	P15238	bacterioph	517	69	3.9	597	1	SILL_PANTR	P07265	saccharomyc
445	70	4.0	298	1	JAMI_BOVIN	Q9xt56	bos taurus	518	69	3.9	644	1	HOB0_DROME	Q951h0	pan troglod
446	70	4.0	403	1	TRPB_ACICA	P16706	acinetobact	519	69	3.9	661	1	NX2_HUMAN	P12258	drosophila
447	70	4.0	421	1	EPC_MOUSE	Q91097	mus musculus	520	69	3.9	715	1	ADSV_MOUSE	Q9u140	homo sapien
448	70	4.0	536	1	YEN1_SCHPO	P06336	mus musculus	521	69	3.9	715	1	NU88_HUMAN	Q60604	mus musculus
449	70	4.0	542	1	EAAL_BOVIN	O13695	schizosacch	522	69	3.9	741	1	INCE_HUMAN	Q99567	homo sapien
450	70	4.0	576	1	ILIR_MOUSE	P46411	bos taurus	523	69	3.9	756	1	NRG2_MOUSE	P56974	mus musculus
451	70	4.0	611	1	VEI_PAPVE	P13504	mus musculus	524	69	3.9	919	1	VP39_YEAST	Q9ng87	homo sapien
452	70	4.0	742	1	NU88_RAT	P11328	europcan el	525	69	3.9	1049	1	VP39_YEAST	Q97468	saccharomyc
453	70	4.0	810	1	CAN3_CHICK	O08658	rattus norv	526	69	3.9	1109	1	HMDH_ASPT	Q9y7d2	aspargillus
454	70	4.0	837	1	GCSR_MOUSE	Q92177	gallus gall	527	69	3.9	1327	1	TKN1_HUMAN	O62947	rattus norv
455	70	4.0	1040	1	AXOI_RAT	P40223	mus musculus	528	69	3.9	1442	1	PTC1_CHICK	Q95271	gallus gall
456	70	4.0	1097	1	PGDR_RAT	Q22063	rattus norv	529	69	3.9	1656	1	ATCB_YEAST	Q90693	gallus gall
457	70	4.0	1162	1	LEPR_MOUSE	Q05030	rattus norv	530	69	3.9	2132	1	PGCA_MOUSE	Q12674	saccharomyc
458	70	4.0	1214	1	SIP1_HUMAN	P48356	mus musculus	531	69	3.9	2196	1	MOR2_SCHPO	Q9hdv6	schizosacch
459	70	4.0	1215	1	SIP1_MOUSE	O60315	homo sapien	532	69	3.9	4563	1	APB_HUMAN	P04114	homo sapien
460	70	4.0	1456	1	RRO_PVXHB	Q9r097	mus musculus	533	68.5	3.9	240	1	CD7_HUMAN	P09564	homo sapien
461	70	4.0	1456	1	RRO_PVXHB	Q07630	potato viru	534	68.5	3.9	268	1	YHC6_YEAST	P37740	saccharomyc
462	70	4.0	1461	1	NEO1_HUMAN	P17779	potato viru	535	68.5	3.9	296	1	YFC1_ECOLI	F87768	escherichia
463	70	4.0	1461	1	AL52_HUMAN	Q92859	homo sapien	536	68.5	3.9	310	1	SDC1_HUMAN	P18827	homo sapien
464	70	4.0	1722	1	LW75_MESAU	Q96q42	homo sapien	537	68.5	3.9	329	1	YQG1_CABEL	Q09272	caenorhabdi
465	70	4.0	2004	1	YP73_VERPE	Q920p9	mesocricetu	538	68.5	3.9	335	1	PSG2_HUMAN	P11465	homo sapien
466	69.5	3.9	270	1	NFAM_HUMAN	Q8zdj2	yersinia pe	539	68.5	3.9	338	1	MDHM_PIG	P00346	sus scrofa
467	69.5	3.9	284	1	SHOE_HUMAN	Q8net5	homo sapien	540	68.5	3.9	366	1	OXAA_MYCTU	Q77vc3	mycobacteri
468	69.5	3.9	295	1	AROE_CHLTE	Q86520	homo sapien	541	68.5	3.9	407	1	LMP1_CRIGR	P49129	cricketul
469	69.5	3.9	327	1	EFB1_XENLA	Q8kbh8	chlorobium	542	68.5	3.9	423	1	LMB1_ERPER	Q8zas9	yersinia pe
470	69.5	3.9	332	1	Y614_PYRHO	O13097	xenopus lae	543	68.5	3.9	448	1	EX7L_BACSU	P54521	bacillus su
471	69.5	3.9	338	1	MDHM_MOUSE	P08249	mus musculus	544	68.5	3.9	453	1	TRME_BUCMP	O51830	buchnera ap

545	68.5	3.9	458	1	CD4_CERAE	Q08338 cercopithec	618	68	3.8	1147	1	KIN2_YEAST	P13186 saccharomyc
546	68.5	3.9	458	1	CD4_HUMAN	P01730 homo sapien	619	68	3.8	1174	1	PTNL_HUMAN	Q16825 homo sapien
547	68.5	3.9	459	1	SPAK_BACSU	P33113 bacillus su	620	68	3.8	1194	1	CHS4_NEUCR	Q01285 neurospora
548	68.5	3.9	464	1	RCAA_HORVU	Q40073 bordeum vul	621	68	3.8	1271	1	YCB1_CAEEL	P19981 caenorhabdi
549	68.5	3.9	497	1	KCS1_MOUSE	Q35173 mus musculu	622	68	3.8	1281	1	MDR3_CRIGR	P23174 cricetus
550	68.5	3.9	524	1	MQ1_CANBF	Q7vr80 candidatus	623	68	3.8	1458	1	PHLX_RABIT	Q05017 oryctolagus
551	68.5	3.9	542	1	IMAI_YEAST	Q02821 saccharomyc	624	68	3.8	1522	1	MRP3_RAT	O88563 rattus norv
552	68.5	3.9	555	1	ILVD_AQUAE	O67009 aquifex aeo	625	68	3.8	1786	1	UVRA_CHLTR	O84337 chlamydia t
553	68.5	3.9	561	1	B105_YEAST	P53744 saccharomyc	626	68	3.8	2124	1	PGCA_RAT	P07897 rattus norv
554	68.5	3.9	584	1	RYK2_DROME	Q9v422 drosophila	627	68	3.8	3341	1	POLG_MCFA	P33515 m genome po
555	68.5	3.9	592	1	PUR2_YEAST	P38009 s bifunctio	628	67.5	3.8	134	1	CYB5_BRAOL	P40934 brassica ol
556	68.5	3.9	601	1	MUTL_LISMO	Q8y788 listeria ap	629	67.5	3.8	148	1	RMP3_HUMAN	O60896 homo sapien
557	68.5	3.9	626	1	HTPG_BUCBP	Q8y693 buchnera mo	630	67.5	3.8	212	1	BROM_ANACO	P14518 ananas como
558	68.5	3.9	654	1	MCPC_BACSU	P54576 bacillus su	631	67.5	3.8	215	1	CIB3_MOUSE	Q8bhk2 mus musculu
559	68.5	3.9	711	1	LCFD_HUMAN	O60488 homo sapien	632	67.5	3.8	221	1	VA36_VACCV	P21059 vaccinia vi
560	68.5	3.9	789	1	SHB4_YEAST	P51534 saccharomyc	633	67.5	3.8	261	1	XVY1_YEAST	P47086 saccharomyc
561	68.5	3.9	827	1	CSG_HALVO	P25062 halobacteri	634	67.5	3.8	322	1	ICOL_MOUSE	Q9jhj8 mus musculu
562	68.5	3.9	831	1	PRUR_CHICK	Q04594 gallus gall	635	67.5	3.8	329	1	GC2_CAVPO	P01862 cavia porce
563	68.5	3.9	906	1	CAD2_HUMAN	P19022 homo sapien	636	67.5	3.8	345	1	EFB1_RAT	P52796 rattus norv
564	68.5	3.9	968	1	CTD1_HUMAN	O60716 homo sapien	637	67.5	3.8	348	1	K2L2_HUMAN	P43627 homo sapien
565	68.5	3.9	972	1	KFMS_HUMAN	P07333 homo sapien	638	67.5	3.8	348	1	OMB1_NEIGO	P18195 neisseria g
566	68.5	3.9	976	1	AMY_BUTFI	P30269 butyrivibri	639	67.5	3.8	348	1	Y479_MYCTU	O11145 mycobacteri
567	68.5	3.9	1043	1	TCF8_MESAU	O60542 mesocricetu	640	67.5	3.8	361	1	SERC_BACHD	Q9kdm4 bacillus ha
568	68.5	3.9	1134	1	YML7_YEAST	Q03735 saccharomyc	641	67.5	3.8	450	1	PUR8_PYRHO	O58582 pyrococcus
569	68.5	3.9	1248	1	DIA1_HUMAN	O60610 homo sapien	642	67.5	3.8	491	1	SYT9_RAT	Q925c0 rattus norv
570	68.5	3.9	1257	1	CAML_HUMAN	P32004 homo sapien	643	67.5	3.8	497	1	KCS1_RAT	O88758 rattus norv
571	68.5	3.9	1466	1	SPA2_YEAST	P23201 saccharomyc	644	67.5	3.8	511	1	KNC1_HUMAN	P48547 homo sapien
572	68.5	3.9	1520	1	PMPD_CHILMU	O9plb0 chlamydia m	645	67.5	3.8	511	1	KNC1_MOUSE	P15388 mus musculu
573	68.5	3.9	1704	1	VILD_DICDI	Q8wq85 dictyosteli	646	67.5	3.8	535	1	SRC_HUMAN	P12931 homo sapien
574	68.5	3.9	3354	1	CADN_HUMAN	Q9h251 homo sapien	647	67.5	3.8	540	1	SRC_MOUSE	P25480 mus musculu
575	68.5	3.9	4349	1	DYHC_FUSSO	P18716 fusarium so	648	67.5	3.8	547	1	CD15_MOUSE	P25918 mus musculu
576	68	3.8	155	1	PCP_HAEIN	P10325 haemophilus	649	67.5	3.8	567	1	IRL1_MOUSE	P14719 mus musculu
577	68	3.8	157	1	PR1_MEDSA	Q43560 medicago sa	650	67.5	3.8	569	1	YB59_MYCPN	P75324 mycoplasma
578	68	3.8	167	1	Y7A1_RICPR	O05960 rickettsia	651	67.5	3.8	570	1	DFAS_ANAPF	Q850c1 anabaena sp
579	68	3.8	221	1	YB31_MYCPN	P75267 mycoplasma	652	67.5	3.8	571	1	ASN2_YEAST	P49090 saccharomyc
580	68	3.8	231	1	YC93_METJA	Q86889 methanococc	653	67.5	3.8	581	1	HPCL_MOUSE	Q9qxe0 mus musculu
581	68	3.8	262	1	CAHD_HUMAN	O8n1q1 homo sapien	654	67.5	3.8	584	1	DAK1_YEAST	P54838 saccharomyc
582	68	3.8	275	1	ICA2_HUMAN	P13598 homo sapien	655	67.5	3.8	587	1	COB8_ONCMY	Q90x85 oncorhynch
583	68	3.8	298	1	HTPX_STRP3	Q8k8k2 streptococ	656	67.5	3.8	615	1	YSPK_CAEEL	P19425 caenorhabdi
584	68	3.8	298	1	HTPX_STRP8	O8p2k0 streptococ	657	67.5	3.8	621	1	Y344_CHLEN	Q9k275 chlamydia p
585	68	3.8	298	1	HTPX_STRPY	Q9ald5 streptococ	658	67.5	3.8	660	1	PKN1_COREF	Q8fui5 chlamydia p
586	68	3.8	340	1	PFTA_ARATH	Q9lx33 a protein f	659	67.5	3.8	697	1	NANB_STRPN	Q54727 streptococ
587	68	3.8	371	1	DP3B_TREPA	O83048 treponema p	660	67.5	3.8	703	1	CNAl_MOUSE	Q8bmd6 mus musculu
588	68	3.8	395	1	SYT8_MOUSE	Q9r0n6 mus musculu	661	67.5	3.8	732	1	ACPH_PIG	P19205 sus scrofa
589	68	3.8	401	1	ASSY_STAAM	Q99vc7 staphylococ	662	67.5	3.8	748	1	SM3B_MOUSE	Q62177 mus musculu
590	68	3.8	401	1	ASSY_STAAM	O89xf2 staphylococ	663	67.5	3.8	790	1	CADI_HUMAN	Q13634 homo sapien
591	68	3.8	409	1	P16P_WHEAT	P09195 triticum ae	664	67.5	3.8	795	1	TLR1_MOUSE	Q9epq1 mus musculu
592	68	3.8	431	1	ORDL_HAEIN	P44732 haemophilus	665	67.5	3.8	837	1	NCM2_HUMAN	O15394 homo sapien
593	68	3.8	514	1	C11A_DASAM	Q92045 dasyatis am	666	67.5	3.8	879	1	YE07_MYCPN	P75377 mycoplasma
594	68	3.8	520	1	LEUI_BRAJA	O89gb0 bradyrhizob	667	67.5	3.8	886	1	DSC1_MOUSE	P55849 mus musculu
595	68	3.8	521	1	ICBA_HUMAN	Q92851 homo sapien	668	67.5	3.8	944	1	CHS2_NEUCR	P30589 neurospora
596	68	3.8	526	1	VP5_ETV10	P07389 bluetongue	669	67.5	3.8	956	1	GLK4_HUMAN	P18099 homo sapien
597	68	3.8	528	1	YE19_SCHPO	O13874 schizosacch	670	67.5	3.8	1036	1	HP12_DEIRA	P13126 deinococcus
598	68	3.8	584	1	MAJ3_YEAST	P38158 saccharomyc	671	67.5	3.8	1062	1	YAI3_HUMAN	Q9Y216 homo sapien
599	68	3.8	595	1	SILL_HUMAN	Q96pq1 homo sapien	672	67.5	3.8	1070	1	PTK7_HUMAN	Q13308 homo sapien
600	68	3.8	632	1	CSX1_SCHPO	O13759 schizosacch	673	67.5	3.8	1072	1	CARB_THETN	Q8rbk0 thermoanaer
601	68	3.8	640	1	GYRB_SPICI	P34031 spiroplasma	674	67.5	3.8	1460	1	PCX1_MOUSE	Q9qycl1 mus musculu
602	68	3.8	649	1	GUND_CLOTM	P04954 clostridium	675	67.5	3.8	1527	1	ARHB_RAT	Q9e867 rattus norv
603	68	3.8	656	1	Y691_RICPR	Q9czn2 rickettsia	676	67.5	3.8	1928	1	LPH_RAT	Q02401 rattus norv
604	68	3.8	680	1	EPG_APPPP	Q9zeu4 apple proli	677	67.5	3.8	2144	1	BP28_HUMAN	Q9H583 homo sapien
605	68	3.8	690	1	PTRB_MORLA	P59470 mus musculu	678	67.5	3.8	2208	1	POLN_MANCV	Q69014 mancheater
606	68	3.8	756	1	RPC2_MOUSE	P59470 mus musculu	679	67.5	3.8	4660	1	LRP2_RAT	P98158 rattus norv
607	68	3.8	789	1	AD07_RAT	O63180 rattus norv	680	67.5	3.8	4660	1	LRP2_RAT	P98158 rattus norv
608	68	3.8	796	1	CORP_SCHPO	O42937 schizosacch	681	67	3.8	131	1	ILL3_MOUSE	P20109 mus musculu
609	68	3.8	814	1	SEFC_SALEN	P33388 salmonella	682	67	3.8	135	1	CYSS_TOBAC	P49099 nicotiana t
610	68	3.8	896	1	RPOP_NEUCR	P33540 neurospora	683	67	3.8	156	1	LI8B_LUPLU	P52779 lupinus lut
611	68	3.8	901	1	VP3_BTIVA	P20608 bluetongue	684	67	3.8	189	1	CD3E_MOUSE	P22646 mus musculu
612	68	3.8	906	1	CAD0_XENLA	P33147 xenopus lae	685	67	3.8	214	1	FLA4_PYRHO	Q58285 pyrococcus
613	68	3.8	912	1	PGCB_BOVIN	Q28062 bos taurus	686	67	3.8	255	1	DAPB_CLOFE	O581e2 clostridium
614	68	3.8	962	1	GUNA_PSEFL	P10476 pseudomonas	687	67	3.8	255	1	YOIX_BACSU	P54535 bacillus su
615	68	3.8	963	1	IRE2_RAT	Q62751 rattus norv	688	67	3.8	282	1	ISPA_BUCAL	P57537 buchnera ap
616	68	3.8	989	1	MERK_RAT	P57097 rattus norv	689	67	3.8	300	1	NANK_HAEIN	P44541 haemophilus
617	68	3.8	997	1	YPX2_CAEEL	Q20256 caenorhabdi	690	67	3.8	316	1	RSP4_TRIGR	P38980 tripneustes

691 67 3.8 320 1 RLUB VIBUO
692 67 3.8 358 1 BLOB METJA
693 67 3.8 371 1 CEL2_HUMAN
694 67 3.8 373 1 REPT_YEAST
695 67 3.8 401 1 ASSY STRAP
696 67 3.8 413 1 HEMO MANSE
697 67 3.8 495 1 CD5_HUMAN
698 67 3.8 501 1 CPJ5 MOUSE
699 67 3.8 524 1 Y395 MYCGE
700 67 3.8 542 1 IMAL_SCHPO

ALIGNMENTS

RESULT 1
LY9_MOUSE
ID LY9_MOUSE STANDARD; PRT; 654 AA.
AC Q01965; Q9ES29; Q9ES35; Q9ES36;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9).
GN LY9 OR Ly-9..
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., AND POLYMORPHISM.
RP STRAIN=129/SV, BALB/c, and C57BL/6; TISSUE=Spleen;
RX MEDLINE=20424510; PubMed=10970093;
RA Tovar V., de la Fuente M.A., Bizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly-9.";
RL Immunogenetics 51:788-793 (2000).
RN [2]
SEQUENCE OF 22-654 FROM N.A., AND SEQUENCE OF 48-59.
RX MEDLINE=92373005; PubMed=1506686;
RA Sandrin M.S., Gumley T.P., Henning M.M., Vaughan H.A., Genez L.J.,
RA Trapani J.A., McKenzie I.F.C.;
RT "Isolation and characterization of cDNA clones for mouse Ly-9.";
RL J. Immunol. 149:1636-1641 (1992).
CC -!- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: LYMPHOCYTES.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC
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CC -----
CC EMBL; AF244131; AAG14997.1; --
CC EMBL; AF244130; AAG14996.1; --
CC EMBL; AF246701; AAG13268.2; --
CC EMBL; AF245117; AAG13268.2; JOINED.
CC EMBL; AF245506; AAG13268.2; JOINED.
CC EMBL; AF245118; AAG13268.2; JOINED.
CC EMBL; AF245507; AAG13268.2; JOINED.
CC EMBL; AF245508; AAG13268.2; JOINED.
CC EMBL; AF245509; AAG13268.2; JOINED.
CC EMBL; AF245510; AAG13268.2; JOINED.
CC EMBL; AF246699; AAG13268.2; JOINED.
CC EMBL; AF246700; AAG13268.2; JOINED.
CC EMBL; M84412; AAG39468.1; --
CC HSP; P08921; 1HNG.
CC MGD; MGI:96885; Ly9.

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;
KW Immunoglobulin domain; Repeat; Polymorphism.
FT SIGNAL 1 47
FT CHAIN 48 654
FT DOMAIN 48 453
FT TRANSMEM 454 474
FT DOMAIN 475 654
FT DOMAIN 48 158
FT DOMAIN 159 243
FT DOMAIN 250 362
FT DOMAIN 353 453
FT DISULFID 172 242
FT DISULFID 178 222
FT DISULFID 376 445
FT DISULFID 382 426
FT CARBOHYD 68 68
FT CARBOHYD 120 120
FT CARBOHYD 231 231
FT CARBOHYD 284 284
FT CARBOHYD 390 390
FT CARBOHYD 412 412
FT CARBOHYD 423 423
FT CARBOHYD 434 434
FT VARIANT 10 10
FT VARIANT 14 14
FT VARIANT 79 79
FT VARIANT 91 91
FT VARIANT 130 130
FT VARIANT 139 139
FT VARIANT 366 366
FT VARIANT 377 377
FT VARIANT 550 550
FT VARIANT 592 592
FT CONFLICT 283 283
FT CONFLICT 499 499
FT CONFLICT 560 560
FT CONFLICT 647 654
SQ SEQUENCE 654 AA; 73142 MW; 1CBBE99708AE8E7 CRC64;
Query Match 20.0%; Score 354.5; DB 1; Length 654;
Best Local Similarity 27.6%; Pred. No. 6.8e-22;
Matches 118; Conservative 52; Mismatches 138; Indels 119; Gaps 16;
Oy 14 LWQL-TGSA---ASGPKELVSGVGVTPFLKSK-VKQVDSIVTFTNTPLVTIQEG 67
Db 238 IWQCTGASRRKTAAG--KTWGLGEPVTLPEFRATRKNNVWVFNTS--VISQRR 293
Oy 68 GTTIIVTQNR-----NRERVDPPDGGYSLKSLKKNDSGIYYVGVSSSQQPSTQRYVL 122
Db 294 GAATADSRKPKGSEERVTSDQSLKISQLKQWEDAGPYHAYVCEASRDSVRHFTL 353
Oy 123 HYVEHLSKPVTKGLQSNKNGTCVTNLTCCWEGEEDVIYTWKALGOAANESNGSLPI 182
Db 354 LVYKRLEKPSVTKSPVHMNGICEVVLTCSDVGGNNVTYTWPLQNKAVMSQCKSLNV 413
Oy 183 SWRWGESDMTFICVARNPVSFNSSPILARKLCEGAADDPDSSMVLCLLLVPLLSLFV 242
Db 414 SWESGEHLNFTCTAHNPVS-NSSQFSSSGTICSG-----PERNRRFWLLLLLLLLMLI 468
Oy 243 LGLFLMFLKRE-----RQEEYIEE-----KKRVDICRETPNICP- 276
Db 469 GGYFILRKQKQCSLATRYQAEVPAEIPETPTGHGQFVLSQRYEKLDMSAKTRHQPT 528
Oy 277 -----HSGENTE---YDTIPHTN----- 291
Db 529 PTSDTSSESATTEDEDEKTRMHSSTANSRNQVYDLVTHQDIAHALAYEGQVEYEAITPYD 588

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QY 292 -----RTIL--KEDPANTYVSTVEIPKK-MENPHSLLMPTTP 326
Db 589 KVDGSMDEDMAYIQVSLNVQGETPLPQKEDSNITVYCSVQPKKTAQTQPDABSPETP 648
QY 327 RLPAVEN 333
Db 649 ----TYEN 652

RESULT 2
LY9_HUMAN STANDARD; PRT; 655 AA.
AC Q9HBG7; Q14775; Q9H4N5; Q9N024;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-lymphocyte surface antigen Ly-9 precursor (Lymphocyte antigen 9)
DE (Cell-surface molecule Ly-9) (CD229 antigen).
OS Ly9.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20424510; PubMed=10970093;
RA Tovar V., de la Fuente M.A., Pizcueta P., Bosch J., Engel P.;
RT "Gene structure of the mouse leukocyte cell surface molecule Ly9.";
RL Immunogenetics 51:788-793(2000).
RN [2]
SEQUENCE OF 32-654 FROM N.A. (ISOFORM 2).
RX MEDLINE=96128248; PubMed=85371117;
RA Sandrin M.S., Henning M.M., Lo M.F., Baker E., Sutherland G.R.,
RA McKenzie I.P.;
RT "Isolation and characterization of cDNA clones for Humly9: the human
RT homologue of mouse Ly9.";
RL Immunogenetics 43:13-19(1996).
RN [3]
SEQUENCE OF 1-151 FROM N.A.
RA Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE OF 99-655 FROM N.A. (ISOFORM 3).
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.P.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May participate in adhesion reactions between T
CC lymphocytes and accessory cells by homophilic interaction.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Experimental confirmation may be lacking for some
CC isoforms;
CC Name=1;
CC IsoId=Q9HBG7-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9HBG7-2; Sequence=VSP_002525;
CC Name=3;
CC IsoId=Q9HBG7-3; Sequence=VSP_002525, VSP_002526, VSP_002527;
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF244129; AAG14995.1; -.
DR EMBL; L42621; AAA92623.1; -.
DR EMBL; AL121985; CAC00580.1; -.

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DR EMBL; AY007142; AAG02002.1; -.
DR Genew; HGNC:6730; LY9.
DR MIM; 600684; -.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Cell adhesion; Antigen; Signal; Transmembrane; Glycoprotein;
KW Immunoglobulin domain; Repeat; Alternative splicing.
FT SIGNAL 1 47
FT CHAIN 48 655
FT DOMAIN 48 454
FT TRANSMEM 455 476
FT DOMAIN 477 655
FT DOMAIN 48 158
FT DOMAIN 159 235
FT DOMAIN 251 363
FT DOMAIN 364 452
FT DISULFID 172 242
FT DISULFID 178 222
FT DISULFID 377 446
FT DISULFID 383 427
FT CARBOHYD 68 68
FT CARBOHYD 95 95
FT CARBOHYD 120 120
FT CARBOHYD 169 169
FT CARBOHYD 173 173
FT CARBOHYD 285 285
FT CARBOHYD 413 413
FT CARBOHYD 424 424
FT VARSPLIC 359 448
FT VARSPLIC 500 513
FT VARSPLIC 524 554
FT CONFLICT 171 171
FT CONFLICT 602 602
SQ SEQUENCE 655 AA; 72107 MW; 9F0A3056D79F80A CRC64;

Query Match 17.9%; Score 318; DB 1; Length 655;
Best Local Similarity 30.3%; Pred. No. 7,6e-19;
Matches 91; Conservative 49; Mismatches 128; Indels 32; Gaps 10;

QY 19 GSAAGSPVKE-LVSGVGAVTFLPK-SKVQVDSIVWTFNTPLVTIOPEGGT---IIVT 73
Db 246 GASRGTTGETVVGVLGPEVTLPLALPACRDTCKVWVLFNTSIISKREEAATADPLIKS 305
QY 74 QNRNRVDFDGGYSLKSLKKNDSGIYVGIYSSSLQQPSTQEVYLVHYHLSPKV 133
Db 306 RDPYKNRVVWSSQDCSLKISQKLTEDAGPYHAYVCEASVTSMTHTLLIYRRLRKPXI 365
QY 134 TWGLQSNKNGTCVTNLCTCMHEGEDVITYWKALQAAANESHGSIPLTISRWGSDMTF 193
Db 366 TWSLRHSEGGICRISLTCSVEDGGNTVMTYTPLOKEAVVSGQESHNVSRSSHNPL 425
QY 194 ICVARNPVSRNFPSPILARKICEGAADPDSSMVLCLLLVPLLSLVGLFLFLPKRE 253
Db 456 TCTASNPVSR-SHQFLSENICSG---PERNTKLWIGLF-LMVCLLCVGFISWCI--- 475
QY 254 RQEEVIEKKRVDICRETPNICPHSGE---NTEYDTIPIHTNRTILKEPANTYVSTVEIP 310
Db 476 -----WKRKGRGCVPAFCSSQAEAPADTPEPTAGHTLYSVLSQG-----YEKLDTP 521

RESULT 3
SLAM_MOUSE
ID SLAM_MOUSE
AC Q9QUM4; Q9QX23;
PRT; 343 AA.

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RX MEDLINE=95342241; PubMed=7617038;
RA Cocks B.G., Chang C.-C.J., Carballido J.M., Yssel H., de Vries J.E.,
RA Aversa G.;
RT "A novel receptor involved in T-cell activation.";
RL Nature 376:260-263 (1995).
CC -!- FUNCTION: HIGH-AFFINITY SELF-LIGAND CONSIDERED TO BE IMPORTANT IN
CC BIDIRECTIONAL T <-> B-CELL STIMULATION. SLAM-INDUCED SIGNAL-
CC TRANSDUCTION EVENTS IN T LYMPHOCYTES ARE DIFFERENT FROM THOSE IN B
CC CELLS. TWO MODES OF SLAM SIGNALING ARE LIKELY TO EXIST: ONE IN
CC WHICH THE INHIBITOR SH2D1A ACTS AS A NEGATIVE REGULATOR AND
CC ANOTHER IN WHICH PROTEIN-TYROSINE PHOSPHATASE 2C (PTPN11)-
CC DEPENDENT SIGNAL TRANSDUCTION OPERATES.
CC -!- SUBUNIT: ITS CYTOPLASMIC DOMAIN INTERACTS WITH SH2 DOMAIN PROTEIN
CC 1A (SH2D1A) THROUGH PART OF ITS SH2 DOMAIN, AND WITH PTPN11.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein; present on the
CC surface of B and T cells.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Long;
CC IsoId=Q13291-1; Sequences=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=Q13291-2; Sequences=VSP_002568, VSP_002569;
CC Name=3; Synonyms=Secreted;
CC IsoId=Q13291-3; Sequences=VSP_002567;
CC -!- TISSUE SPECIFICITY: Constitutively expressed on peripheral blood
CC memory T cells, T-cell clones, immature thymocytes, and a
CC proportion of B-cells, and is rapidly induced on naive T cells
CC after activation.
CC -!- DOMAIN: SH2 DOMAINS USE TO BIND TO PHOSPHOTYROSINE RESIDUES IN A
CC SEQUENCE-SPECIFIC MANNER. IN THIS CASE, HOWEVER, THE SPECIFIC
CC SH2D1A-BINDING SITE IS AROUND THE MOST MEMBRANE-PROXIMAL TYROSINE
CC RESIDUE (TYR-281) OF THE CYTOPLASMIC TAIL, AND PHOSPHORYLATION OF
CC TYR-281 IS NOT REQUIRED FOR BINDING.
CC -!- PTM: PHOSPHORYLATED BY FYN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CDw150 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw150.htm".
CC -----
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CC -----
DR EMBL; U33017; AAA75380.1; -
DR PIR; S58892; S58892.
DR PDB; 1D4T; 10-APR-00.
DR PDB; 1D4W; 04-APR-00.
DR PDB; 1KA6; 28-AUG-02.
DR PDB; 1KA7; 28-AUG-02.
DR Genew; HGNC:10903; SLAMF1.
DR MIM; 603492; -
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0004888; F:transmembrane receptor activity; TAS.
DR GO; GO:0006960; P:antimicrobial humoral response (sensu Inver...); TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor; Signal; Transmembrane; T-cell; Antigen; Glycoprotein;
KW Repeat; Immunoglobulin domain; Phosphorylation; Alternative splicing;
KW 3D-structure. 1 20 POTENTIAL.
FT SIGNAL 21 335 SIGNALING LYMPHOCYTIC ACTIVATION
FT CHAIN 21 335 MOLECULE.
FT FT
FT DOMAIN 21 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 335 CYTOPLASMIC (POTENTIAL).
FT DOMAIN ? 152 IG-LIKE V-TYPE.
FT DOMAIN 144 223 IG-LIKE C2-TYPE.
FT DISULFID 158 228 BY SIMILARITY.

FT DISULFID 164 209 BY SIMILARITY.
FT SITE 281 SH2-BINDING (POTENTIAL).
FT SITE 307 SH2-BINDING (POTENTIAL).
FT SITE 327 SH2-BINDING (POTENTIAL).
FT CARBOHYD 53 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 57 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 102 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 125 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 150 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 155 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 189 N-LINKED (GLCNAC... (POTENTIAL).
FT CARBOHYD 217 N-LINKED (GLCNAC... (POTENTIAL).
FT VARSPLIC 234 Missing (in isoform 3).
FT VARSPLIC 289 /FTID=VSP_002567.
FT VARSPLIC 299 /FTID=VSP_002568.
FT VARSPLIC 335 /FTID=VSP_002569.
SQ SEQUENCE 335 AA; 37231 MW; BPH0F27EA31D8C04 CRC64;
Query Match 10.3%; Score 182.5; DB 1; Length 335;
Best Local Similarity 22.5%; Pred. No. 7e-08;
Matches 82; Conservative 72; Mismatches 129; Indels 81; Gaps 19;
QY 8 LTLIYILM-QLTGSASGP-----VKELVSGVGAFTPL-----KSKVKQVDSIVWT 54
DB 7 LSLTFVLFSLAFGASVGTGGRMMNCPKILRLQSGKVLPLTYERINKSMNKSIIHIVTM 66
QY 55 FNT-----TPLVITQP-EGGTIIVTQNRNRVDVDPGGYSLKSLKNDGIIYVGI 107
DB 67 AKSLNSVENKIVSLDPSEAG-----PPRYLGDYKFFYLENLTLGIRSRKDEGWLMTL 122
QY 108 YSS-SLQOPSTQEVYLVHYEHLSPKVTGWSKNGKTCVTNLTCCMEHGEDVIYTW-- 164
DB 133 EKNVSVQRFCLQ---LRLYEQVSTPEIKVLNKTQENGCTLLIGCTVEGDH-VAYSNSE 178
QY 165 KALQOANESNHSGLPISWRGSDMTFICVARNPVSRNFS--SPILARKLCEGAADDP 222
DB 179 KAGTHPLNPANSHLLSLTLGPHQADNIYICTVSNPISNNSQTFSP-----WPGCRTP 232
QY 223 DSSM-----VLCLLLVPLLLSLFVLGLFLMFLKRRQBEYIE---EKRVVIC 268
DB 233 SETRPWAVYAGLGGVIMILMVILQ-----LRRRGKTNHYQTTVKKSLLTY 281
QY 269 RETPNICPHSGENTYDTRIPHTNRILKEDPANTVY--STVEIPKPMENPHSL-----LT 321
DB 282 AQVQKGP---LQKKLDSFP-----AQDPCTTIIVATEPVPESVQETNSITVYASVT 331
QY 322 MPDT 325
DB 332 LPES 335
RESULT 5
CD2_MOUSE STANDARD; PRT; 344 AA.
ID CD2_MOUSE
AC P08320; O61394;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE T-cell surface antigen CD2 precursor (T-cell surface antigen
DE T11/Leu-5) (LFA-2) (LFA-3 receptor).
GN CD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=87276135; PubMed=2440689;
RA Sewell W.A., Brown M.H., Fink P.J., Kozak C.A., Crumpton M.J.;
RT "The murine homologue of the T lymphocyte CD2 antigen: molecular

cloning, chromosome assignment and cell surface expression.";
 Eur. J. Immunol. 17:1015-1020(1987).
 [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=88004738; PubMed=2820751;
 RA Clayton L.K., Sayre P.H., Novotny J., Reinherz E.L.;
 RT "Murine and human T11 (CD2) cDNA sequences suggest a common signal
 transduction mechanism";
 RL Eur. J. Immunol. 17:1367-1370(1987).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALE/c; TISSUE=Liver;
 RX MEDLINE=88144486; PubMed=2894031;
 RA Diamond D.J., Clayton L.K., Sayre P.H., Reinherz E.L.;
 RT "Exon-intron organization and sequence comparison of human and murine
 T11 (CD2) genes";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1615-1619(1988).
 [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=88140313; PubMed=3257775;
 RX Yagita H., Okumura K., Nakauchi H.;
 RA "Molecular cloning of the murine homologue of CD2. Homology of the
 molecule to its human counterpart T11.";
 RL J. Immunol. 140:1321-1326(1988).
 [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6; TISSUE=Hematopoietic;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.L., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RN INTERACTION WITH CD2AP.
 RX MEDLINE=98412662; PubMed=9741631;
 RA Dustin M.L., Olszowy M.W., Holdorf A.D., Li J., Bromley S., Desai N.,
 RA Widder P., Rosenberger F., van der Merwe P.A., Allen P.M., Shaw A.S.;
 RT "A novel adaptor protein orchestrates receptor patterning and
 cytoskeletal polarity in T-cell contacts.";
 RL Cell 94:667(1998).
 CC -!- FUNCTION: CD2 interacts with lymphocyte function-associated
 antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T
 cells and other cell types. CD2 is implicated in the triggering
 of T-cells, the cytoplasmic domain is implicated in the
 signalling function.
 CC -!- SUBUNIT: Interacts with CD2AP.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC
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 or send an email to license@isb-sib.ch).

CC DR Y00023; CAA68258.1; --
 DR EMBL; X06143; CAA29500.1; --
 DR EMBL; M19807; AAA37393.1; --
 DR EMBL; M19799; AAA37393.1; JOINED.
 DR EMBL; M19801; AAA37393.1; JOINED.
 DR EMBL; M19803; AAA37393.1; JOINED.
 DR EMBL; M19805; AAA37393.1; JOINED.
 DR EMBL; M19834; AAA37397.1; --
 DR EMBL; BC053731; AAA53731.1; --
 DR PIR; I49585; I49585.
 DR HSSP; P08921; I464.
 DR MGI; 88320; Cd2.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0004872; F:receptor activity; ISS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF05790; CD2; 1.
 DR PROSITE; PS0835; IG LIKE; FALSE NEG.
 DR Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
 KW Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 22 T-CELL SURFACE ANTIGEN CD2.
 FT CHAIN 23 344 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 23 203 POTENTIAL.
 FT TRANSMEM 204 229 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 230 344 IG-LIKE V-TYPE.
 FT DOMAIN 23 121 IG-LIKE C2-TYPE.
 FT DOMAIN 122 202 PRO-RICH.
 FT DOMAIN 276 343 BY SIMILARITY.
 FT DISULFID 133 197 BY SIMILARITY.
 FT DISULFID 140 180 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 94 94 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 99 99 Y -> T (IN REF. 3).
 FT CONFLICT 128 128 M -> V (IN REF. 3 AND 4).
 FT CONFLICT 139 139 T -> I (IN REF. 4).
 FT CONFLICT 175 175 N -> A (IN REF. 3).
 FT CONFLICT 175 175 N -> S (IN REF. 4).
 FT CONFLICT 191 191 K -> N (IN REF. 2).
 FT CONFLICT 192 192 M -> T (IN REF. 3 AND 4).
 SQ SEQUENCE 344 AA; 38414 MW; CFI212FCBD1444450 CRC64;
 Query Match 8.1%; Score 144; DB 1; Length 344;
 Best Local Similarity 21.4%; Pred. No. 0.00012;
 Matches 72; Conservative 56; Mismatches 132; Indels 76; Gaps 16;
 QY 12 YILWLTGSAASGPVKELV-GSVGAVT--FPLKSKVKQVDSIVWNTTPTLVITIQEGG 68
 DB 10 FLLPFLSGKGCACRDNETINGVLGHTLNIPNQMTDDIDEVRV-----RRG 58
 QY 69 TIIVTQNR-----ERVDPDGGYSIKLSK-LKKNDSGIYVYGVYSSSLQPSSTQYV 121
 DB 59 TLVAEFKPKPKPFLISETYEVLANG-SLKIKKPMRNDSGIYVWVGTNGMTREKDLDD 117
 QY 122 LHVTEHLSKPKVMTGLQSNKNGTCV-TNLTCCMHGEEDVIYTWKALQAAANSHNGSIL 180
 DB 118 VRILERSVKPMI-----HWECPTTLTCAVLQGTDFELKLYQ--GETLLNS-----L 162
 QY 181 P----ISWRWGESDMTFFICVARNPVSRRPSSPILARKLCEGAADPDSSWLLCL----- 231
 DB 163 PQKNMSYQWNTLNAPFKCEAINPVSKSRMEV-----NCFEKLSPYVTVGVGAG 213
 QY 232 -LLVPLLLSLFVLGLFWLFLKREQEYIEBKRVDICRETPNICPHSGENTYDTIPT 290
 DB 214 GLLVLLVLFVFI----FCICRKRNRNRKDEELIKASRTS-----TVERCPKHS 261
 QY 291 NRTILKEDPANTVSTVEIPKKNPHSLTMDPTP 326
 DB 262 T-----PAAQAQNSVALQAPPPPGHILQTFGHP 290

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heiton E., Kretzmer M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ÅNGSTRÖMS) OF 25-206.
 RX MEDLINE=95086863; PubMed=7994575;
 RA Bodian D.L., Jones E.Y., Harlos K., Stuart D.I., Davis S.J.,
 RA "Crystal structure of the extracellular region of the human cell
 RT adhesion molecule CD2 at 2.5-Å resolution."
 RL Structure 2:755-766(1994).
 RN [10]
 RP STRUCTURE BY NMR OF 25-129.
 RX MEDLINE=9434885; PubMed=7915183;
 RA Withka J.M., Wyss D.F., Wagner G., Arulanandam A.R.N., Reinherz E.L.,
 RA Recny M.A.,
 RT "Structure of the glycosylated adhesion domain of human T lymphocyte
 RL glycoprotein CD2."
 RL Structure 1:69-81(1993).
 RN [11]
 RP STRUCTURE BY NMR OF 25-129.
 RX MEDLINE=95381065; PubMed=7544493;
 RA Wyss D.F., Choi J.S., Li J., Knoppers M.H., Willis K.J.,
 RA Arulanandam A.R., Smolyar A., Reinherz E.L., Wagner G.,
 RT "Conformation and function of the N-linked glycan in the adhesion
 RL domain of human CD2."
 RL Science 269:1273-1278(1995).
 RN [12]
 RP MUTAGENESIS.
 RX MEDLINE=88039075; PubMed=2444890;
 RA Peterson A., Seed B.,
 RT "Monoclonal antibody and ligand binding sites of the T cell
 RL erythrocyte receptor (CD2)."
 RL Nature 329:842-846(1987).
 RN [13]
 RP CD59-BINDING DATA.
 RX MEDLINE=92311658; PubMed=1377404;
 RA Hahn W.C., Menu E., Bothwell A.L.M., Sims P.J., Bierer B.E.,
 RT "Overlapping but nonidentical binding sites on CD2 for CD58 and a
 RL second ligand CD59."
 RL Science 256:1805-1807(1992).
 CC -!- FUNCTION: CD2 interacts with lymphocyte function-associated
 CC antigen (LFA-3) and CD48/BCM1 to mediate adhesion between T
 CC cells and other cell types. CD2 is implicated in the triggering
 CC of T-cells, the cytoplasmic domain is implicated in the
 CC signaling function.
 CC -!- SUBUNIT: Interacts with CD2AP (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD2 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd2.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M16445; AAA51738.1; -
 DR EMBL; M14362; AAA35571.1; -
 DR EMBL; M16336; AAA51946.1; -
 DR EMBL; M19806; AAA53095.1; -
 DR EMBL; M19798; AAA53095.1; JOINED.
 DR EMBL; M19800; AAA53095.1; JOINED.
 DR EMBL; M19802; AAA53095.1; JOINED.
 DR EMBL; M19804; AAA53095.1; JOINED.
 DR EMBL; X07871; CAA30721.1; -
 DR EMBL; X07872; CAA30721.1; JOINED.
 DR EMBL; X07873; CAA30721.1; JOINED.
 DR EMBL; X07874; CAA30721.1; JOINED.
 DR EMBL; AL135798; CAC14840.1; -
 DR EMBL; BC033583; AAH33583.1; -
 DR PIR; A28967; RWIUC2.
 DR PDB; 1CDB; 15-OCT-94.
 DR PDB; 1HNF; 07-FEB-95.
 DR PDB; 1GYA; 08-NOV-96.
 DR PDB; 1L2Z; 20-NOV-02.
 DR GlycoSuiteDB; P06729; -
 DR Genew; HGNC:1639; CD2.
 DR MIM; 186930; -
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0004872; F:receptor activity; NAS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 DR GO; GO:0016337; P:cell-cell adhesion; NAS.
 DR GO; GO:0006917; P:induction of apoptosis; TAS.
 DR GO; GO:0045768; P:positive regulation of anti-apoptosis; NAS.
 DR GO; GO:0045580; P:regulation of T-cell differentiation; NAS.
 DR GO; GO:0042110; P:T-cell activation; TAS.
 DR InterPro; IPR008424; CD2.
 DR Pfam; PF05790; CD2; 1.
 DR PROSITE; PS50835; IG LIKE; FALSE NEG.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Antigen; Transmembrane;
 KW Cell adhesion; Repeat; Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 24
 FT CHAIN 25 351 T-CELL SURFACE ANTIGEN CD2.
 FT DOMAIN 25 209 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 210 235 POTENTIAL.
 FT DOMAIN 236 351 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 25 128 IG-LIKE V-TYPE.
 FT DOMAIN 129 209 IG-LIKE C2-TYPE.
 FT DOMAIN 61 75 LFA-3 (CD58) BINDING REGION 1.
 FT DOMAIN 106 120 LFA-3 (CD58) BINDING REGION 2.
 FT DOMAIN 282 338 PRO-RICH.
 FT DISULFID 139 203 BY SIMILARITY.
 FT DISULFID 146 186 BY SIMILARITY.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 266 266 Q -> H (in dbSNP:699738).
 FT MUTAGEN 67 67 /FtId=VAR_017104.
 FT MUTAGEN 70 70 K->R: LOSS OF LFA-3 BINDING.
 FT MUTAGEN 110 110 Q->K: LOSS OF LFA-3 BINDING.
 FT MUTAGEN 111 110 Y->D: LOSS OF LFA-3 AND CD59 BINDING.
 FT CONFLICT 287 287 D->H: LOSS OF LFA-3 AND CD59 BINDING.
 FT CONFLICT 339 351 G -> A (IN REF. 3).
 FT CONFLICT 339 351 HGAAENSLSPSSN -> MGQKTHCPPLIKDRNCLFQ
 (IN REF. 3).
 Query Match 7.5%; Score 133.5; DB 1; Length 351;
 Best Local Similarity 22.7%; Pred. No. 0.00093;
 Matches 68; Conservative 52; Mismatches 105; Indels 75; Gaps 15;
 Qy 28 ELVSGVGVATFLKS--KVKQVDSIW--TFNTTTLVLTQPEGGIIVTQNRNRVDF 83
 Db 32 ETWALGQDINLIPSFQMSDDIDDKWETSDDKIKIAQFRKEKTF---KEDTYKL-F 87

FT STRAND 177 183
 FT TURN 184 185
 FT STRAND 186 192
 SQ SEQUENCE 344 AA; 38414 MW; 41BAED392CE16356 CRC64;

Query Match
 Best Local Similarity 7.3%; Score 130; DB 1; Length 344;
 Matches 65; Conservative 51; Mismatches 112; Indels 62; Gaps 13;

QY 12 YILWLTGSA---SGPVKELVSGGAVTFPLKVKQVDSIVTFNTPLVITQPG 67
 DB 10 FLFLSLSSKACDRDSTGVMGALGH-GINLINIENFQMTDDIDVRW-----BR 56
 QY 68 GTTIIVTQNRNRERVDPPGGY-----SLKSLKKNKDSIYVGVYSSLSQPSQEVV 121
 DB 57 GSTLVAEFKKMPFLKSGAFELANGDLKIKULTRDDSGTYNVYISTNGTRILDKALD 116
 QY 122 LHYEHLSPKPVMTGLQSNKNGTCV-----TNLTCMEHGEEDVIYTWKALQAAANESHNG 177
 DB 117 LRILEVSKPMIYWECSNATLTCEVLEGTVDVELKLYQKEHL-----RSLRQKT----- 165
 QY 178 SILPISNRGESDMTFCIVARNPVSRNFSPIARLKLCEGADDDPSMWLLCLLLVPL- 236
 DB 166 ----MSYQWTLNLRAPFKCAVNRVQSEMEVV-----NCPEKGLPLYLIIVGSAG 212
 QY 237 -LLSLVLGLFLWFL-----KREROEYIEEK-KRVDICRETPNICPHS 278
 DB 213 GLLLVFFGALFIFCCKRKKRNRKGELEIKASRMSTVERGPK--PHS 260

RESULT 9
 CD48_MOUSE
 ID CD48_MOUSE STANDARD; PRT; 240 AA.
 AC P18181;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MRC OX-45 surface antigen precursor (BCM1 surface antigen) (BLAST-1)
 DE (CD48) (HM48-1).
 GN CD48 OR BCM-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=90278362; PubMed=1693656;
 RA Wong Y.W., Williams A.F., Kingmore S.F., Seldin M.F.;
 RT "Structure, expression, and genetic linkage of the mouse BCM1 (OX45
 RT or Blast-1) antigen. Evidence for genetic duplication giving rise to
 RT the BCM1 region on mouse chromosome 1 and the CD2/LFA3 region on
 RT mouse chromosome 3.";
 RL J. Exp. Med. 171:2115-2130 (1990).
 RN [2]
 RP SEQUENCE OF 23-40.
 RX MEDLINE=93018850; PubMed=1383383;
 RA Kato K., Koyanagi M., Okada H., Takanashi T., Wong Y.W., Williams A.F.,
 RA Okumura K., Yagita H.;
 RT "CD48 is a counter-receptor for mouse CD2 and is involved in T cell
 RT activation.";
 RL J. Exp. Med. 176:1241-1249 (1992).
 CC -!- FUNCTION: LIGAND FOR CD2. MIGHT FACILITATE INTERACTION BETWEEN
 CC ACTIVATED LYMPHOCYTES. PROBABLY INVOLVED IN REGULATING T-CELL
 CC ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
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 CC -----
 DR EMBL; X53526; CAA37604.1; -;
 DR EMBL; X17501; CAA35542.1; -;
 DR PIR; J0143; J0143.
 DR MGI; 88339; Cd48.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Antigen; Repeat; Signal; Immunoglobulin domain; Glycoprotein;
 KW Lipoprotein; GPI-anchor.
 FT SIGNAL 1 22
 FT CHAIN 23 217
 FT PROPEP 218 240
 FT DOMAIN 29 125
 FT DOMAIN 129 209
 FT LIPID 217 217
 FT DISULFID 151 193
 FT CARBOHYD 32 32
 FT CARBOHYD 38 38
 FT CARBOHYD 70 70
 FT CARBOHYD 136 136
 FT CARBOHYD 186 186
 FT CARBOHYD 203 203
 SQ SEQUENCE 240 AA; 27383 MW; F3BF6987A9E9C71E CRC64;

Query Match
 Best Local Similarity 7.1%; Score 126.5; DB 1; Length 240;
 Matches 52; Conservative 45; Mismatches 125; Indels 21; Gaps 8;

QY 7 CLTIYILMQLTGSAAAGPVKELVSGGAVTFPL-KSKVKQVDSIVTFNTPLVITQ 65
 DB 9 CLVLELLPLGTGTFQGHISIPDINATGTSNVTLKHKDPLGPKYRIITWLTKNQKILEYN 68
 QY 66 EGGTIIIVTONRERVDPPGGYISLKLKKNDSIYVGVYSSLSQPSQSTQ-EYVLHV 124
 DB 69 YNSTKTIFESEFKGRVYLEENNGALHISNRKEDKGYIMRV-----LRETNELKITLEV 124
 QY 125 YEHLSKPKVTMLQSNKNGTCVNTLTCMEHGEEDVIYTWKALQAAANESHGSIPLSW 184
 DB 125 FDPVPKPSIEINKTEASTDSCHLRLSC--EVKDHVDYTWYESSGPPKSPGVLDIV 182
 QY 185 RWGESDMTFCIVARNPVSRN-----FSPPI-LARK--LCEGAADDDPSMWLLCLLLVPL 236
 DB 183 TPQNKSTFTYTCQVSNPVSKNDTVYFTPLCDLARSSGVCWTA-----TWLVVTTLIHRI 237
 QY 237 LLS 239
 DB 238 LLT 240

RESULT 10
 CEAL_HUMAN
 ID CEAL_HUMAN STANDARD; PRT; 526 AA.
 AC P13688;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Carcinoembryonic antigen-related cell adhesion molecule 1 precursor
 DE (Biliary glycoprotein 1) (BGP-1) (Antigen CD66) (CD66a antigen).
 GN CEACAM1 OR BGP OR BGPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88320535; PubMed=2457922;
 RA Hinoda Y., Neumaier M., Hefta S.A., Drzeniek Z., Wagener C.,

QY 68 GTIIVTQ-----NRRNRVDPDGGYSLKSLKLNKDSGIYVGYSSSL-QQPSTOR 119
 Db 81 GYALGTQATPGPANGSRETI-YPNA--SLIQVNTQNDTGFYTLQVKSIDLNEBQTQ 137
 QY 120 YLVHVEHLSPKPVWGLQNKNGTCTVNTLTCMHEGEEDVIYTWKALQAQANESHGSI 179
 Db 138 F--HVYPELPKPGPISNNPNVEDKDAVPTC--EPETQDTTVLWMI-----NNQS 184
 QY 180 LPISRW----GESDWTFFICVAR-----NVSNSFPSPILARKLCEG-----A 218
 Db 185 LPVSPLQLNGNRTTLTUSVTRNDTGPVECEIQNPVSANRSDPV-TLVNTYGPDPPTIS 243
 QY 219 ADD-----PDSMVLCLLL--VPLLSSLFVLGLFWFLKREOEYIEKKRVDCRETP 272
 Db 244 PSDTYRPGANLSLSCVAASNPAPQYSLWINGTF-----QOSTQELFI-----P 287
 QY 273 NI-CPHSGENTFY--DTIPHTNRTILK 296
 Db 288 NITVNSGSYTHANNSVTGCNRTTVK 314

RESULT 11

CEA6_HUMAN STANDARD; PRT; 344 AA.
 AC P40199; Q14920;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Carcinoembryonic antigen-related cell adhesion molecule 6 precursor
 DE (Normal cross-reacting antigen) (Nonspecific crossreacting antigen)
 DE (CD66c antigen).
 GN CEA6 OR NCA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCB_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89122014; PubMed=3220478;
 RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
 RT "Carcinoembryonic antigen family: characterization of cDNAs coding
 RT for NCA and CEA and suggestion of nonrandom sequence variation in
 RT their conserved loop-domains.";
 RL Genomics 3:59-66(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung carcinomas;
 RX MEDLINE=88106638; PubMed=3337731;
 RA Tawaragi Y., Oikawa S., Matsuoka Y., Kosaki G., Nakazato H.;
 RT "Primary structure of nonspecific crossreacting antigen (NCA), a
 RT member of carcinoembryonic antigen (CEA) gene family, deduced from
 RT cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 150:89-96(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalón D.K., Muzny N.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily, CEA family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD66c entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd66c.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M29541; ARA59915.1; -;
 CC EMBL; M18728; ARA59907.1; -;
 CC EMBL; BC005008; AAH05008.1; -;
 CC Genew; HGNC:1818; CEACAM6.
 CC MIM; 163980; -;
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0007267; P:cell-cell signaling; TAS.
 CC DR GO; GO:0007185; P:signal transduction; TAS.
 CC DR InterPro; IPR007110; IG-like.
 CC DR InterPro; IPR003598; Ig_c2.
 CC DR Pfam; PF00047; Ig; 3.
 CC DR SMART; SM00408; IGC2; 1.
 CC DR PROSITE; PS50835; IG_LIKE; 2.
 CC DR Immunoglobulin domain; Antigen; Signal; Glycoprotein; GPI-anchor;
 KW Repeat; Lipoprotein.
 FT SIGNAL 1 34
 FT CHAIN 35 320
 FT PROPEP 321 344
 FT LIPID 320 320
 FT DOMAIN 35 142
 FT DOMAIN 145 232
 FT DOMAIN 237 314
 FT DISULFID 167 215
 FT DISULFID 259 299
 FT CARBOHYD 104 104
 FT CARBOHYD 111 111
 FT CARBOHYD 115 115
 FT CARBOHYD 152 152
 FT CARBOHYD 173 173
 FT CARBOHYD 197 197
 FT CARBOHYD 224 224
 FT CARBOHYD 256 256
 FT CARBOHYD 274 274
 FT CARBOHYD 288 288
 FT CARBOHYD 292 292
 FT CARBOHYD 309 309
 FT CONFLICT 138 138
 FT CONFLICT 239 239
 SQ SEQUENCE 344 AA; 37237 MW; 4322C5D6E25849F5 CRC64;
 Query Match 7.0%; Score 124.5; DB 1; Length 344;
 Best Local Similarity 22.4%; Pred. No. 0.0051;
 Matches 75; Conservative 35; Mismatches 118; Indels 107; Gaps 16;
 QY 53 WFTNTPLVTIQ-----PPGGTII-----VTQNR-----NRRVD----- 82
 Db 28 WNPPTAKLTIETPFNVAEGKGLLAHLNLPQNRIGYSWYKGVDRDGNLSIVGYVIGTQ 87
 QY 83 --FPDGGY-----SLKSLKKNDSGIYVGYSSSL-QQPSTQVVLHVYHLS 129
 Db 88 QATPGPAYSGRETIYPNASLLIQNTQNDTGFYTLQVKSIDLNEBQTQF--HVYPELP 145

QY 130 KPKVTNGLQSNKGTCTVTLNLCMEHGEEDVITYTKALQQAANESHNGSILPISWRW---- 186
 Db 146 KPSISNNPNVEDDAVFTC--EPEVQNTTYLWV-----NGQSLPVSRELQLS 194
 QY 187 -GESDWTFI-----CVARNPVSNFSGSPILARKLC-----EGAAADDPSS 225
 Db 195 NGNMTLLTSLVKRNDAGSYECIQNPASANRSDPVTNLVLYGPDVPTTSPSKANYRPGEN 254
 QY 226 MVLCLLL--VPLLSSFLVLGLFLFKRKEROBEYTEEKRVDCRETENI----- 274
 Db 255 LNLSCHAASNPAQVSWFNGTF-----QOSTQLFT-----PNITVNNSGSYM 298
 QY 275 CPHSGENTYDITPHNTRILKEDPANTVYSTVEI 309
 Db 299 COAHNSATGLNRTTMTITVSGSAPVLSAVATGVI 333

RESULT 12

CDXAR HUMAN STANDARD; PRT; 365 AA.
 AC P78310; O00694;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coxsackievirus and adenovirus receptor precursor (Coxsackievirus B-
 CXADR OR CAR.
 GN Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97190109; PubMed=9036860;
 RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,
 RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;
 RT "Isolation of a common receptor for Coxsackie B viruses and
 RT adenoviruses 2 and 5";
 RL Science 275:1320-1323(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97250541; PubMed=9096397;
 RA Tomko R.P., Xu R., Philipson L.;
 RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C
 RT adenoviruses and group B coxsackieviruses";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20008750; PubMed=10543405;
 RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,
 RA Bowles N.E.;
 RT "Genomic organization and chromosomal localization of the human
 RT Coxsackievirus B-adenovirus receptor gene";
 RL Hum. Genet. 105:354-359(1999).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;
 RT "Sequence and expression of CXADR, the human gene for the
 RT coxsackievirus and adenovirus receptor";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RP Anderson B., Tomko R., Andersson K., Darban H., Oncu D., Mizra M.,
 RA Sollerbrant K., Sonhammer E., Philipson L.;
 RT "Putative regulatory domains in the human and mouse CAR genes";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Cervix;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Bottrifield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND
 CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 CC
 CC EMBL; Y07593; AAC68868.1; -;
 CC EMBL; U07116; AAC51234.1; -;
 CC
 CC EMBL; AF169366; AAF05908.1; -;
 CC EMBL; AF169360; AAF05908.1; JOINED.
 CC EMBL; AF169361; AAF05908.1; JOINED.
 CC EMBL; AF169362; AAF05908.1; JOINED.
 CC EMBL; AF169363; AAF05908.1; JOINED.
 CC EMBL; AF169364; AAF05908.1; JOINED.
 CC EMBL; AF169365; AAF05908.1; JOINED.
 CC EMBL; AF200465; AAF24344.1; -;
 CC EMBL; AF242865; AAG01088.1; -;
 CC EMBL; AF242862; AAG01088.1; JOINED.
 CC EMBL; AF242864; AAG01088.1; JOINED.
 CC EMBL; BC003684; AAH03684.1; -;
 CC EMBL; BC010536; AAH10536.1; -;
 CC PDB; 1EAJ; 13-JUL-01.
 CC PDB; 1F5W; 08-NOV-00.
 CC PDB; 1KAC; 24-NOV-99.
 CC Genew; HGNC:2559; CXADR.
 CC MIM; 602621; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004872; F:receptor activity; TAS.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003598; IG_c2.
 CC Pfam; PF00047; IG_2.
 CC SMART; SM00408; IGC2; 1.
 CC PROSITE; PS50835; IG_LIKE; 2.
 KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 365
 FT DOMAIN 20 237
 FT TRANSMEM 238 258
 FT DOMAIN 259 365
 FT DOMAIN 20 134
 FT DOMAIN 141 228
 FT DISULFID 41 120
 FT DISULFID 162 212
 FT CARBOHYD 106 106
 FT CARBOHYD 201 201
 SQ SEQUENCE 365 AA; 40029 MW; AB01C6346CB7FE64 CRC64;
 Query Match 6.7%; Score 119.5; DB 1; Length 365;

Best Local Similarity 21.2%; Pred. No. 0.014;
Matches 62; Conservative 47; Mismatches 124; Indels 59; Gaps 12;
QY 68 GTTIVTQNRNRVDFPDGGYSKLSKLNKDSGIYVYSSLOQPTQEVVHLVYEH 127
Db 89 GRVHFTSN-----DLKSGDASINVNLQSLDITGYQCKVKA-----PGVANKKIHLVV- 137
QY 128 LSKPKVTMGLOSNGKT-----CVTNLTCCMEHGEEDVIYTKALGOAANESHNGSLTPTS 183
Db 138 LVKPS---GARCVDGSEIGDFKIKCEPKESLPQYEWQKLSQK-----MPTS 187
QY 184 W-----RWGESDMTFICVARNPVRNFSSPILARKLCEGAADDPDSSNVLLC 230
Db 188 WLAEMTSSVISVKNASSEYSGTVCVRNVG---SDQCLRL-----NVVPSNKAFLIA 240
QY 231 LLVAPLLLSLFLVGLFLWFLKREQEYIEEKKRVDCRETNPICPHSGENTYDTIPHT 290
Db 241 GALTGLTLLALGLLIIFCCKRREKEVHHDIREDVPP--PKSRTSTARSYIGSN 298
QY 291 NRTILKEDPAN-----TVYSTV-----EIPKMPENPHSLTMDPTPLFA 330
Db 299 HSLGSMSPNMEGYSKTYNQVPSDFERTQSPFLPAKVAAPNLSMGA 350

RESULT 13
A33 HUMAN STANDARD; PRT; 319 AA.
AC Q99795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cell surface A33 antigen precursor (Glycoprotein A33).
GN GPA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97396159; PubMed=9245713;
RA Heath J.K., White S.G., Johnstone C.N., Catimel B., Simpson R.J.,
RA Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA Burgess A.W.,
RT "The human A33 antigen is a transmembrane glycoprotein and a novel
RT member of the immunoglobulin superfamily".
RL Proc. Natl. Acad. Sci. U.S.A. 94:469-474 (1997).
RN [2]
RN POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=97396159; PubMed=9245713;
RA Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA Simpson R.J.,
RT "Characterization of posttranslational modifications of human A33
RT antigen, a novel palmitoylated surface glycoprotein of human
RT gastrointestinal epithelium.";
RL Biochem. Biophys. Res. Commun. 236:682-686 (1997).
CC -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC epithelium and in 95% of colon cancers.
CC -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC CARBOHYDRATE.
CC -!- PTM: Palmitoylated.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

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CC EMBL; U79725; AAC50957.1; -;
CC Genew; HGNC:4445; GPA33.
DR MIM; 602171; -;
DR GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR GO; GO:0004872; P:receptor activity; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
KW Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW Transmembrane; Signal; Antigen.
FT SIGNAL 1 21
FT CHAIN 22 319 CELL SURFACE A33 ANTIGEN.
FT DOMAIN 22 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 257 319 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 134 IG-LIKE V-TYPE.
FT DOMAIN 140 227 IG-LIKE C2-TYPE.
FT DOMAIN 258 261 POLY-CYS.
FT DISULFID 43 117 POTENTIAL.
FT DISULFID 146 222 POTENTIAL.
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 35632 MW; 9BFC7AAF45C2408E CRC64;
Query Match 6.6%; Score 116.5; DB 1; Length 319;
Best Local Similarity 22.6%; Pred. No. 0.022;
Matches 73; Conservative 50; Mismatches 123; Indels 77; Gaps 15;
QY 13 ILWQL-----TGSAA--GPVKELVSGVGAATPPL-----KSKVKQVDSIVTWFNT 57
Db 8 VLWTLCAVRVTDVAISVETPDVLRASQGSKVTLPCTVHTSTSSREGLIQWDLKLLTH-- 65
QY 58 TPLVTIOPEGTTIIVTQNRNRVDFPDGG-----YSLKSLKLNKDSGIYVYSSLSQ 113
Db 66 TERVVIFPFNNKNIYHGLYKRVNISNNAEQSDASITIDQLTWADNGTYECSVLSMDL 125
QY 114 QPSTOEYV-LHYVEHLSKPKVTMGLOSNGKTCTVN--LTCCMEHGEEDVIYTWK--A 166
Db 126 EGNYSRVLLVLPVPSKPE--CGIEGE---TIIGNIQLTCSKESPTPOYSWKYNI 180
QY 167 LGOAANESHNGSLIPISRWGESDMT--FICVARNPVRNFSSPILARKLCEGAADDPDS 224
Db 181 LNQEPLAQASGPVSLKNISTDTSYICTSSNEBGTQFCNITVAVR-----SPSM 233
QY 225 SWVLLCLLVPLLLSLVGLFLWF-----LKR 252
Db 234 NVALYVGIVGVAALIIIIIIYCCCRKDDNTEDKEDARPNEAYEPEPEQLRELSR 293
QY 253 EROEE--YIEKKRVDCRETNP 273
Db 294 EREEDDYRQEQR-STGRESFD 315
RESULT 14
CEA5 HUMAN STANDARD; PRT; 702 AA.
AC P06731;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Carcinoembryonic antigen-related cell adhesion molecule 5 precursor
DE (Carcinoembryonic antigen) (CEA) (Meconium antigen 100) (CD66
DE antigen).
GN CEACAM5 OR CEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90258861; PubMed=2342461;
 RA Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
 RT Hassauer M., Shively J.E., von Kleist S., Zimmermann W.;
 RT "Cloning of the complete gene for carcinoembryonic antigen: analysis
 of its promoter indicates a region conveying cell type-specific
 expression";
 RL Mol. Cell. Biol. 10:2738-2748(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89122014; PubMed=3220478;
 RA Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
 RT "Carcinoembryonic antigen family: characterization of cDNAs coding
 for NCA and CEA and suggestion of non-random sequence variation in
 their conserved loop-domains.";
 RL Genomics 3:59-66(1988).
 RN [4]
 RP SEQUENCE OF 5-702 FROM N.A.
 RX MEDLINE=87128144; PubMed=3814146;
 RA Okawa S., Nakazato H., Kosaki G.;
 RT "Primary structure of human carcinoembryonic antigen (CEA) deduced
 from cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 142:511-518(1987).
 RN [5]
 RP SEQUENCE OF 331-702 FROM N.A.
 RX MEDLINE=87204247; PubMed=3033671;
 RA Zimmermann W., Ortlieb B., Friedrich R.; von Kleist S.;
 RT "Isolation and characterization of cDNA clones encoding the human
 carcinoembryonic antigen reveal a highly conserved repeating
 structure";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Found in adenocarcinomas of endodermally
 derived digestive system epithelium and fetal colon.
 CC -!- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 kDa
 CC COMPRISING 60* CARBOHYDRATE.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. CEA family.
 CC -!- SIMILARITY: Contains 7 immunoglobulin-like domains.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD66e entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd66e.htm".
 CC -----
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DR EMBL; M16234; AAA51972.1; -.
 DR PIR; A36319; A36319.
 DR PDB; 1B07; 04-JUL-00.
 DR Genew; HGNC:1817; CEACAM5.
 DR MIM; 114890; -.
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG; 6.
 DR PROSITE; PS50835; IG LIKE; 6.
 KW Immunoglobulin domain; Lipoprotein; GPI-anchor;
 KW Membrane; Signal; Repeat; 3D-structure.
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 FT FT
 FT PROPEP 686 702
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 FT CONFLICT 320 320 MISSING (IN REF. 4).
 SQ SEQUENCE 702 AA; 76795 MW; 6299AE26CDBDB5C CRC64;
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 Best Local Similarity 21.2%; Pred. No. 0.084;
 Matches 66; Conservative 36; Mismatches 111; Indels 99; Gaps 14;
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 DB 81 GYVIGTQQATPGPAYSGREIIYPNA--SLIIQIIQNDTGFYTLHKVSDLVNEATGQF 138
 QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALQAAANESNGSL 180
 DB 139 --RVYPELPKPSISNNKPKVEDKDAVFTC--EPETQDATYLVWV-----NQSL 185
 QY 181 PISRW-----GESDMT-----FICVARNPVSRNFSPIILARKL----- 214
 DB 186 PVSPLQLSNGNRTLTLENTVNDTASYKCEQNFVARRSDSVILNVLYGPDAPFTISPL 245
 QY 215 -----CEGAADDDPSMWLLCLLLVPLLLSLFVLGLFLWFKRRQREYEE 261
 DB 246 NTSYRSGENLNLSC-AASNP-----PAQYSWFVNGTF-----QQSTQELFI-- 286

Db 183 NGESE---GDRKLS--EGNRTLNTRNDTGPVCETRNPVSVNRSDP 230

Search completed: August 18, 2004, 15:51:35
Job time : 18 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:52:59 ; Search time 54 Seconds
(without alignments)
1752.841 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 335

Sequence: 1 MAGSPTCLTIYLWLQGS.....PHSLTMDPTRLPAYENVI 335

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1980s:*

3: Geneseq2000s:*

4: Geneseq2000s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	335	100.0	335	3	AAY70431 Human cel
3	335	100.0	335	3	AAY44609 Human mvo
4	335	100.0	335	4	AAU29119 Human PRO
5	335	100.0	335	4	AAAB7548 Human PRO
6	335	100.0	335	4	AAAB7321 APEX-1. B
7	335	100.0	335	4	AAAB6522 Human PRO
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543	335	335	100.0	335	7	ABO28210	Human sec
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552	335	335	100.0	335	7	ABO28210	Human sec
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558	335	335	100.0	335	7	ABO28210	Human sec
559	335	335	100.0	335	7	ABO28210	Human sec
560	335	335	100.0	335	7	ABO28210	Human sec
561	335	335	100.0	335	7	ABO28210	Human sec
562	335	335	100.0	335	7	ABO28210	Human sec
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537	91	27.2	91	4	AAM77190	Human bon	610	8	2.4	360	6	ABO11142	Human sec
538	91	27.2	91	4	AAM64367	Human bra	611	8	2.4	360	6	ABR66760	Human sec
539	91	27.2	91	4	ABG58815	Human liv	612	8	2.4	360	6	ABO15973	Human sec
540	91	27.2	91	5	ABG46203	Human pep	613	8	2.4	360	6	ABO13679	Human sec
541	86	25.7	90	3	ABG32404	Human sec	614	8	2.4	360	6	ABO47399	Human sec
542	88	20.3	124	2	AA12645	Human 5	615	8	2.4	360	6	ABU65582	Human sec
543	33	9.9	33	2	AAW67933	Fragment	616	8	2.4	360	6	ABO07430	Human PRO
544	37	8.1	28	2	AAW67932	Fragment	617	8	2.4	360	6	ABO03617	Human PRO
545	19	5.7	114	3	AAM87990	Human imm	618	8	2.4	360	6	ABR67065	Human sec
546	11	3.3	11	7	ADC89505	Human nat	619	8	2.4	360	6	ABO15668	Human sec
547	11	3.3	12	7	ADC89504	Human nat	620	8	2.4	360	6	ABU55949	Human sec
548	11	3.3	16	7	ADC89506	Human nat	621	8	2.4	360	6	ABU55277	Human PRO
549	9	2.7	66	3	ADG25088	Arabidops	622	8	2.4	360	6	ABU95222	Novel hum
550	9	2.7	66	3	ADG25088	Arabidops	623	8	2.4	360	6	ABU71125	Human PRO
551	9	2.7	456	4	ABG25025	Novel hum	624	8	2.4	360	6	ABO07735	Human PRO
552	8	2.4	15	2	AA13308	Naturally	625	8	2.4	360	6	ABR69976	Human sec
553	8	2.4	26	4	AA174404	Desmoglei	626	8	2.4	360	6	ABR69309	Human sec
554	8	2.4	105	4	AA80619	Environme	627	8	2.4	360	6	ABO01450	Human PRO
555	8	2.4	122	2	AAW37871	Human pro	628	8	2.4	360	6	ABU81252	Human PRO
556	8	2.4	172	4	AAE27244	Human EXM	629	8	2.4	360	6	ABR60049	Human sec
557	8	2.4	194	4	AAW40751	Human pol	630	8	2.4	360	6	ABR67784	Human sec
558	8	2.4	289	3	AA193912	A human h	631	8	2.4	360	6	ABR65172	Human sec
559	8	2.4	306	6	ABU24508	Protein e	632	8	2.4	360	6	ABR68394	Human sec
560	8	2.4	310	6	ADA55489	Human pro	633	8	2.4	360	6	ABR71806	Human sec
561	8	2.4	360	2	AA13381	Amino aci	634	8	2.4	360	6	ABU85286	Human PRO
562	8	2.4	360	3	ADC78533	Human PRO	635	8	2.4	360	6	ABU88976	Human sec
563	8	2.4	360	4	AA80249	Human PRO	636	8	2.4	360	6	ABU83056	Human sec
564	8	2.4	360	4	AU29037	Human PRO	637	8	2.4	360	6	ABU94912	Novel hum
565	8	2.4	360	4	AA138965	Human pol	638	8	2.4	360	6	ABU90460	Novel hum
566	8	2.4	360	6	ABU58413	Human PRO	639	8	2.4	360	6	ABU83971	Human sec
567	8	2.4	360	6	ABU71627	Human PRO	640	8	2.4	360	6	ABU93622	Novel hum
568	8	2.4	360	6	ABU87961	Novel hum	641	8	2.4	360	6	ABR64867	Human sec
569	8	2.4	360	6	ABU84276	Human sec	642	8	2.4	360	6	ABR68699	Human sec
570	8	2.4	360	6	ABR66150	Human sec	643	8	2.4	360	6	ABO06515	Human sec
571	8	2.4	360	6	ABR65540	Human sec	644	8	2.4	360	6	ABR92060	Human sec
572	8	2.4	360	6	ABU99480	Human sec	645	8	2.4	360	6	ABU56944	Human PRO
573	8	2.4	360	6	ABU82719	Human PRO	646	8	2.4	360	6	ABU64536	Human sec
574	8	2.4	360	6	ABU89840	Novel hum	647	8	2.4	360	6	ABU85896	Novel hum
575	8	2.4	360	6	ABU71482	Human PRO	648	8	2.4	360	6	ABU67382	Human sec
576	8	2.4	360	6	ABR68089	Human sec	649	8	2.4	360	6	ABU82183	Novel hum
577	8	2.4	360	6	ABU96142	Novel hum	650	8	2.4	360	6	ABU87194	Human PRO
578	8	2.4	360	6	ABU92573	Human sec	651	8	2.4	360	6	ABU83666	Human sec
579	8	2.4	360	6	ABO08650	Human sec	652	8	2.4	360	6	ABO08040	Human PRO
580	8	2.4	360	6	ABO02702	Human sec	653	8	2.4	360	6	ABO14902	Human sec
581	8	2.4	360	6	ABR74856	Human sec	654	8	2.4	360	6	ABU81751	Novel hum
582	8	2.4	360	6	ABR94618	Human sec	655	8	2.4	360	6	ABU65915	Novel hum
583	8	2.4	360	6	ABU85591	Human PRO	656	8	2.4	360	6	ABR59744	Human sec
584	8	2.4	360	6	ABU98751	Novel hum	657	8	2.4	360	6	ABU93932	Novel hum
585	8	2.4	360	6	ABU97966	Novel hum	658	8	2.4	360	6	ABU99785	Novel hum
586	8	2.4	360	6	ABU91672	Novel hum	659	8	2.4	360	6	ABR66455	Human sec
587	8	2.4	360	6	ABU71928	Human sec	660	8	2.4	360	6	ABR90873	Human sec
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589	8	2.4	360	6	ABU86206	Human sec	662	8	2.4	360	6	ABU79182	Human PRO
590	8	2.4	360	6	ABU67419	Human sec	663	8	2.4	360	6	ABU86511	Human sec
591	8	2.4	360	6	ABU80447	Human PRO	664	8	2.4	360	6	ABU86816	Novel hum
592	8	2.4	360	6	ABO01811	Novel hum	665	8	2.4	360	6	ABU94605	Human PRO
593	8	2.4	360	6	ABR99365	Human sec	666	8	2.4	360	6	ABO04532	Human PRO
594	8	2.4	360	6	ABR98755	Human sec	667	8	2.4	360	6	ABR70281	Human sec
595	8	2.4	360	6	ABO16278	Human sec	668	8	2.4	360	6	ABU98446	Human PRO
596	8	2.4	360	6	ABR92178	Human sec	669	8	2.4	360	6	ABR65845	Human sec
597	8	2.4	360	6	ABO18819	Human sec	670	8	2.4	360	6	ABR64562	Human sec
598	8	2.4	360	6	ABR78240	Human sec	671	8	2.4	360	6	ABU79487	Human PRO
599	8	2.4	360	6	ABU84976	Novel hum	672	8	2.4	360	6	ABU92878	Human sec
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601	8	2.4	360	6	ABO11447	Human sec	674	8	2.4	360	6	ABU91057	Novel hum
602	8	2.4	360	6	ABO02092	Human sec	675	8	2.4	360	6	ABU90150	Novel hum
603	8	2.4	360	6	ABU54384	Human sec	676	8	2.4	360	6	ABO09565	Human sec
604	8	2.4	360	6	ABU88666	Novel hum	677	8	2.4	360	6	ABO10837	Human sec
605	8	2.4	360	6	ABU83361	Human sec	678	8	2.4	360	6	ABR70891	Human sec
606	8	2.4	360	6	ABO06162	Novel hum	679	8	2.4	360	6	ABU87499	Human PRO
607	8	2.4	360	6	ABR59198	Human sec	680	8	2.4	360	6	ABU91367	Human PRO
608	8	2.4	360	6	ABO09260	Human sec	681	8	2.4	360	6	ABU84581	Human sec
609	8	2.4	360	6	ABO19124	Novel hum	682	8	2.4	360	6	ABR69671	Human sec

683 8 2.4 360 6 ABU80048 Human PRO
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 687 8 2.4 360 6 ABO08955 Human sec
 688 8 2.4 360 6 ABO10523 Human sec
 689 8 2.4 360 6 ABU95532 Human PRO
 690 8 2.4 360 6 ABU96741 Novel hum
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 697 8 2.4 360 6 ABR95533 Human sec
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ALIGNMENTS

RESULT 1

AAAY66701
 ID AAY66701 standard; protein; 335 AA.

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 AC AAY66701;

XX
 DT 05-APR-2000 (first entry)

XX
 DE Membrane-bound protein PRO1138.

XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW Pharmaceutical; receptor immunoadhesin; gene mapping.

XX
 OS Homo sapiens.

XX
 PN WO9963088-A2.

XX
 PD 09-DEC-1999.

XX
 PF 02-JUN-1999; 99WO-US012252.

XX
 PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.

PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.

PR 04-JUN-1998; 98US-0088021P.

PR 04-JUN-1998; 98US-0088025P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

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PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088730P.

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PR 10-JUN-1998; 98US-0088740P.

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PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

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 PR 22-JUN-1998; 98US-0090246P.
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 PR 22-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.
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 PR 24-JUN-1998; 98US-0090538P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 25-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090678P.
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 PR 26-JUN-1998; 98US-0090862P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
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 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 07-JUL-1998; 98US-0091982P.
 PR 09-JUL-1998; 98US-0092182P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095321P.
 PR 04-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095916P.
 PR 10-AUG-1998; 98US-0095929P.
 PR 10-AUG-1998; 98US-0096012P.

CC disease. MP-7 proteins may also be used for cellular regulation of immune
CC cell types, cell cycle, differentiation of multipotent cells, and
CC modulation of cell-cell interactions. MP-7 may also be used in screening
CC assays to identify agonists and antagonists and to raise antibodies
XX
SQ Sequence 335 AA;

Query Match 100.0%; Score 335; DB 3; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTLYILWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVVNTTTP 60
DB 1 MAGSPCTCLTLYILWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVVNTTTP 60
QY 61 VTIOPEGGTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSSSQQSTQBY 120
DB 61 VTIOPEGGTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSSSQQSTQBY 120
QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGOANESHNGSIL 180
DB 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGOANESHNGSIL 180
QY 181 PISRWGESDMTFICVARNPVSRNFSPIARLCEGAADDPDSSMVLCLLLVPLLSL 240
DB 181 PISRWGESDMTFICVARNPVSRNFSPIARLCEGAADDPDSSMVLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDCRETNICPHSGENTYDTPHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDCRETNICPHSGENTYDTPHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKQENPHSLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKQENPHSLTTPDTPRLPAYENVI 335

RESULT 4

ID AAU29119 standard; protein; 335 AA.
AC AAU29119;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #96.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000US-0201370S.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015284.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS46020.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumors, such as prostate and breast tumors, in mammals and to
screen for modulators of the compounds.

Claim 11; Fig 192; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, rectal, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders

SQ Sequence 335 AA;

Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTLYILWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVVNTTTP 60
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QY 61 VTIOPEGGTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSSSQQSTQBY 120
DB 61 VTIOPEGGTIIVTQNRNRERVDPPGGYSLKSLKKNDSGIYVYGVYSSSSSQQSTQBY 120
QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGOANESHNGSIL 180

Db 121 VLHYEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALQQAANESHNGSIL 180
 QY 181 PISRWGESDMTFICVARNPVSRNFPSSPILARKLCEGAADDDSSWLLCLLLVPLLSL 240
 Db 181 PISRWGESDMTFICVARNPVSRNFPSSPILARKLCEGAADDDSSWLLCLLLVPLLSL 240
 QY 241 FVLGLFLWFLKREQEYIEEKKRVDICRETPNICPHSGENTYDTIPTHNRTILKEDPA 300
 Db 241 FVLGLFLWFLKREQEYIEEKKRVDICRETPNICPHSGENTYDTIPTHNRTILKEDPA 300
 QY 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335
 Db 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335

RESULT 5

AAB87548
 ID AAB87548 standard; protein; 335 AA.

AC AAB87548;
 XX 15-MAY-2001 (first entry)
 XX Human PRO1138.
 XX Human; PRO protein; mapping.
 XX Homo sapiens.
 XX WO200116318-A2.
 XX 08-MAR-2001.
 XX 24-AUG-2000; 2000WO-US023328.

PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX WPI: 2001-183260/18.
 XX N-PSDS; AAF92080.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 XX biology, including use as hybridization probes, and in chromosome and
 XX gene mapping.

XX Claim 12; Fig 46; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and
 XX transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 XX anti-PRO antibodies are useful for preparation of a medicament useful in
 XX the treatment of a condition which is responsive to the PRO protein,
 XX agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 XX employed as molecular weight markers for protein electrophoresis. The PRO
 XX coding sequence has applications in molecular biology, including use as
 XX hybridisation probes, and in chromosome and gene mapping

XX Sequence 335 AA;
 SQ Query Match 100.0%; Score 335; DB 4; Length 335;
 Best Local Similarity 100.0%; Pred. No. 1.6e-314;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSPTCLTIYIIWOLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
 Db 1 MAGSPTCLTIYIIWOLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
 QY 61 VTIQEGGTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYSSLSQOPSTQY 120
 Db 61 VTIQEGGTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYSSLSQOPSTQY 120
 QY 121 VLHYEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALQQAANESHNGSIL 180
 Db 121 VLHYEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALQQAANESHNGSIL 180
 QY 181 PISRWGESDMTFICVARNPVSRNFPSSPILARKLCEGAADDDSSWLLCLLLVPLLSL 240
 Db 181 PISRWGESDMTFICVARNPVSRNFPSSPILARKLCEGAADDDSSWLLCLLLVPLLSL 240
 QY 241 FVLGLFLWFLKREQEYIEEKKRVDICRETPNICPHSGENTYDTIPTHNRTILKEDPA 300
 Db 241 FVLGLFLWFLKREQEYIEEKKRVDICRETPNICPHSGENTYDTIPTHNRTILKEDPA 300
 QY 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335
 Db 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335

RESULT 6

AAB47321
 ID AAB47321 standard; protein; 335 AA.

XX AAB47321;
 XX 29-AUG-2001 (first entry)
 XX APEX-1.

XX Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
 KW extracellular domain; immunoglobulin-like domain; Ig-like structure;
 KW N-glycosylation site; transmembrane domain; cytoplasmic domain;
 KW SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
 KW Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
 KW cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
 KW inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
 KW myocardial inflammation; pericardial inflammation; osteoarthritis;
 KW osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
 KW inflammation; cancer; autoimmune disease; graft rejection;
 KW graft versus host disease; systemic lupus erythematosus.

XX Homo sapiens.

XX Key Location/Qualifiers
 XX Peptide 1..22
 XX Protein /label= Signal peptide
 XX Domain /label= Mature APEX-1
 XX 226..250
 XX /label= Transmembrane domain

XX WO200146260-A2.

XX 28-JUN-2001.

XX 22-DEC-2000; 2000WO-US034963.

XX 23-DEC-1999; 99US-0172025P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Starling GC, Finger J;
XX WPI; 2001-418044/44.
DR N-PSDB; AAC66114.
XX Novel Antigen presenting cell expression protein useful for treating
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT disease and atopic dermatitis.
XX Claim 3; Fig 2; 112pp; English.
XX The sequences given in AAB47321-23 represent antigen presenting cell
CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC comprise an extracellular domain having one immunoglobulin (Ig)-like
CC structure and N-glycosylation site, a transmembrane domain, and a
CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC and antibodies are useful in the study, diagnosis, prevention and
CC treatment of disease associated with the presence of an APEX protein
CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC diseases, graft rejections, graft versus host reaction and systemic lupus
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC markers on APCs or APEX expressing cells, the ability to elicit the
CC generation of antibodies and as targets for various therapeutic
CC modalities. APEX proteins are also useful for identifying and isolating
CC ligand that bind APEX
SQ Sequence 335 AA;
Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314; Mismatches 0; Indels 0; Gaps 0;
Matches 335; Conservative 0;
QY 1 MAGSPCTCLTLYILWQLTGSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTNTPTPL 60
Db 1 MAGSPCTCLTLYILWQLTGSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTNTPTPL 60
QY 61 VTIQEGGTTIVTQNRNRRVDFPDGGYSLKLSKLKNDGSIYVYGVYSSSLQQPSTQY 120
Db 61 VTIQEGGTTIVTQNRNRRVDFPDGGYSLKLSKLKNDGSIYVYGVYSSSLQQPSTQY 120
QY 121 VLHVYHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSIL 180
Db 121 VLHVYHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSIL 180
QY 181 PISWRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSWVLLCLLVPLLSL 240
Db 181 PISWRWGESDMTFICVARNPVSRNFSPIIARKLCEGAADDPDSSWVLLCLLVPLLSL 240
QY 241 FVLGLFLWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTNRTILKEDPA 300
QY 301 NTVYSTVPIPKOMENPHSLTTPDTPRLPAYENVI 335
Db 301 NTVYSTVPIPKOMENPHSLTTPDTPRLPAYENVI 335
RESULT 7
AAB65224
ID AAB65224 standard; protein; 335 AA.
XX AAB65224;
XX AAB65224;
DT 02-APR-2001 (first entry)
XX Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
DE
XX

KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
OS Homo sapiens.
XX WO200073454-A1.
PN 07-DEC-2000.
PD 30-MAR-2000; 2000WO-US008439.
PF 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2001-032160/04.
DR N-PSDB; AAF44186.
XX PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX Claim 12; Fig 171; 935pp; English..
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX Sequence 335 AA;
SQ Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1	MAGSPTCLLLIYLWLTGSAAGPVKELVGVGGAVTPEPLSKVKQVDSIYVTFNTTPL 60
Db 1	MAGSPTCLLLIYLWLTGSAAGPVKELVGVGGAVTPEPLSKVKQVDSIYVTFNTTPL 60
QY 61	VTIQPEGGIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYVGYSSSLQQPSTOBY 120
Db 61	VTIQPEGGIIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYVGYSSSLQQPSTOBY 120
QY 121	VLVHYEHLSPKVTMGLQNKNGTCVTNLTCCMEHGEEDVIYVTKALGOANESHNGSIL 180
Db 121	VLVHYEHLSPKVTMGLQNKNGTCVTNLTCCMEHGEEDVIYVTKALGOANESHNGSIL 180
QY 181	PISWRGSDMTFICVARNPVGRNFPSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 181	PISWRGSDMTFICVARNPVGRNFPSSPILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
QY 241	FVLGLFWLFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
Db 241	FVLGLFWLFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
QY 301	NTVYSTVEIPKKOVNPHSLTTPDTPRLFAYENVI 335
Db 301	NTVYSTVEIPKKOVNPHSLTTPDTPRLFAYENVI 335

RESULT 8

ABG95873

ID ABG95873 standard; protein; 335 AA.

XX AC ABG95873;

XX DT 10-DEC-2002 (first entry)

XX DE Human secreted/transmembrane protein PRO1138.

XX Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX Homo sapiens.

XX PN US2002119130-A1.

XX PD 29-AUG-2002.

XX PF 06-DEC-2001; 2001US-00006867.

XX PR 29-OCT-1997; 97US-0063435P.

XX PR 22-APR-1998; 98US-0082797P.

XX PR 29-APR-1998; 98US-0083495P.

XX PR 15-MAY-1998; 98US-0085579P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088740P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

XX PR 11-JUN-1998; 98US-0088863P.

XX PR 12-JUN-1998; 98US-0089105P.

XX PR 16-JUN-1998; 98US-0089514P.

XX PR 17-JUN-1998; 98US-0089653P.

XX PR 19-JUN-1998; 98US-0089952P.

XX PR 22-JUN-1998; 98US-0090246P.

XX PR 24-JUN-1998; 98US-0090444P.

XX PR 25-JUN-1998; 98US-0090689P.

XX PR 25-JUN-1998; 98US-0090695P.

XX PR 26-JUN-1998; 98US-0090862P.

PR 02-JUL-1998;	98US-0091628P.
PR 10-AUG-1998;	98US-0096012P.
PR 17-AUG-1998;	98US-0096757P.
PR 18-AUG-1998;	98US-0096949P.
PR 18-AUG-1998;	98US-0096959P.
PR 26-AUG-1998;	98US-0097954P.
PR 26-AUG-1998;	98US-0097971P.
PR 26-AUG-1998;	98US-0097979P.
PR 01-SEP-1998;	98US-0098749P.
PR 10-SEP-1998;	98US-0099741P.
PR 10-SEP-1998;	98US-0099763P.
PR 10-SEP-1998;	98US-0099792P.
PR 10-SEP-1998;	98US-0099812P.
PR 10-SEP-1998;	98US-0099815P.
PR 16-SEP-1998;	98US-0100627P.
PR 16-SEP-1998;	98US-0100662P.
PR 17-SEP-1998;	98US-0100683P.
PR 17-SEP-1998;	98US-0100684P.
PR 17-SEP-1998;	98US-0100930P.
PR 22-SEP-1998;	98US-0101279P.
PR 23-SEP-1998;	98US-0101475P.
PR 24-SEP-1998;	98US-0101738P.
PR 24-SEP-1998;	98US-0101743P.
PR 30-SEP-1998;	98US-0101916P.
PR 30-SEP-1998;	98US-0102570P.
PR 06-OCT-1998;	98US-0103449P.
PR 08-MAR-1999;	99WO-US005028.
PR 14-MAY-1999;	99WO-US010733.
PR 02-JUN-1999;	99WO-US012252.
PR 01-SEP-1999;	99WO-US020111.
PR 15-SEP-1999;	99WO-US021090.
PR 15-SEP-1999;	99WO-US021194.
PR 22-DEC-1999;	99WO-US030720.
PR 18-FEB-2000;	2000WO-US004341.
PR 18-FEB-2000;	2000WO-US004342.
PR 22-FEB-2000;	2000WO-US004414.
PR 01-MAR-2000;	2000WO-US005601.
PR 30-MAR-2000;	2000WO-US008439.
PR 22-MAY-2000;	2000WO-US014042.
PR 02-JUN-2000;	2000WO-US015264.
PR 23-AUG-2000;	2000WO-US023522.
PR 24-AUG-2000;	2000WO-US023328.
PR 10-NOV-2000;	2000WO-US030873.
PR 01-DEC-2000;	2000WO-US032378.
PR 20-DEC-2000;	2000WO-US034956.
PR 28-FEB-2001;	2001WO-US006520.
PR 01-MAR-2001;	2001WO-US006666.
PR 30-MAY-2001;	2001WO-US017443.
PR 01-JUN-2001;	2001WO-US017800.
PR 20-JUN-2001;	2001WO-US019692.
PR 29-JUN-2001;	2001WO-US021066.
PR 09-JUL-2001;	2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.

N-PSDB; ABS74400.

New isolated secreted and transmembrane PRO polypeptide useful for

modulating biological activity of a cell, or for treating sports-related

joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 46; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as

ABG95851-ABG95934 or their associated signal peptide, or a sequence of an

extracellular domain of the proteins with their associated signal peptide

or lacking its associated signal peptide. Also included are the nucleic

acid sequences encoding the polypeptides and the proteins.

CC acids encoding the proteins, vectors, host cells, fusion proteins and
CC antibodies which specifically bind to the proteins. The proteins are
CC useful for detecting a polypeptide designated as A, B, C or D in a sample
CC suspected of containing an A, B, C or D polypeptide, by contacting the
CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
CC conjugate in the sample, where the formation of the conjugate is
CC indicative of the presence of an A, B, C or D polypeptide in the sample,
CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
CC H or I polypeptide is labeled with a detectable label or is attached to a
CC solid support. The proteins are useful for linking a bioactive molecule
CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
CC or I, or antibodies against them are useful for modulating a biological
CC activity of a cell expressing a polypeptide designated as A, B, C or D or
CC E, F, G, H, or I. The cell is killed. The proteins are useful for
CC identifying agonists or antagonists, for the preparation of a medicament
CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention

XX Sequence 335 AA;

Query Match 100.0%; Score 335; DB 5; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGSPTCLTLYILMOLTSAAAGPVKELVSGVGAATFPLKSKVKQVDSIYVTFNTTPL 60
DB 1 MAGSPTCLTLYILMOLTSAAAGPVKELVSGVGAATFPLKSKVKQVDSIYVTFNTTPL 60
QY 61 VTIOPEGGTHIYVTONRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSLQQPSTQRY 120
DB 61 VTIOPEGGTHIYVTONRNRVDFPDGGYSLKSLKKNDSGIYVGYSSSLQQPSTQRY 120
QY 121 VLHVYHLSPKVTWGLQSKNGKTCVNTLTCMEHGEEDVIYTKALGOAANESHNGSL 180
DB 121 VLHVYHLSPKVTWGLQSKNGKTCVNTLTCMEHGEEDVIYTKALGOAANESHNGSL 180
QY 181 PLSRWGESDMTFCIVARNPVRNFSPPILARKLCEGAADDPDSSVLLCLLVPLLSSL 240
DB 181 PLSRWGESDMTFCIVARNPVRNFSPPILARKLCEGAADDPDSSVLLCLLVPLLSSL 240
QY 241 FVLGLPLWPKRQEYIEKKRVDICRETNICPHSGENTYDTIPTNRTILKEDPA 300
DB 241 FVLGLPLWPKRQEYIEKKRVDICRETNICPHSGENTYDTIPTNRTILKEDPA 300
QY 301 NTIVYSTVEIPKMWENPHSLTTPDTPRLFAYENVI 335
DB 301 NTIVYSTVEIPKMWENPHSLTTPDTPRLFAYENVI 335

RESULT 9

ABU58495

ID ABU58495 standard; protein; 335 AA.

XX

AC ABU58495;

XX 15-APR-2003 (first entry)
DT Human PRO polypeptide #96.
XX
DE Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
XX US2003027272-A1.
PN
XX 06-FEB-2003.
PD
XX 21-JUN-2002; 2002US-00176492.
PF
XX 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.

PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
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PR	02-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
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PR	24-JUN-1998;	98US-0090535P.	PR	30-SEP-1998;	98US-0102487P.
PR	24-JUN-1998;	98US-0090540P.	PR	30-SEP-1998;	98US-0102570P.
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PR	02-JUL-1998;	98US-0091478P.			
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Db	1	MAGSPTCLTIYILWQLTGSAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTPL	60		
Qy	61	VTIQEGGTIIVTQNRNRERVDFFDGGVSLKSLKKNDSIGIYVGYSSLSQPSTOEY	120		
Db	61	VTIQEGGTIIVTQNRNRERVDFFDGGVSLKSLKKNDSIGIYVGYSSLSQPSTOEY	120		
Qy	121	VLHYEHLSPKVTMGLOSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHSIL	180		
Db	121	VLHYEHLSPKVTMGLOSNKNGTCVTNLTCMEHGEDVITYWKALGOAANESHSIL	180		
Qy	181	PISWRGESDMTFCIVARNPVSRNFFSPILARKLCEGAADPDSSMWLLCLLLVPLLSL	240		
Db	181	PISWRGESDMTFCIVARNPVSRNFFSPILARKLCEGAADPDSSMWLLCLLLVPLLSL	240		
Qy	241	FVLGLFLWFLKREQEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA	300		

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Db      241  ||||| 241 FVLGLFLWFLKRRQEQEYIEKKRVDICRETPNICPHSGENTGYDTPIHTNRTILKEDPA 300
Qy      301  NTVYSTVEIPKKMENPHSLLTMPDTPRLPAYENVI 335
Db      301  NTVYSTVEIPKKMENPHSLLTMPDTPRLPAYENVI 335

RESULT 10
ID ABU88043 standard; protein; 335 AA.
XX ABU88043;
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XX 07-JUL-2003 (first entry)
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XX Novel human secreted and transmembrane protein PRO1138.
XX
XX Human; secreted and transmembrane protein: PRO; gene therapy;
XX tumour necrosis factor-alpha release; TNF-alpha release;
XX chondrocyte proliferation; chondrocyte differentiation; tumour;
XX adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX
XX Homo sapiens.
XX
XX US2003032127-A1.
XX
XX 13-FEB-2003.
XX
XX 26-JUN-2002; 2002US-00183012.
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XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
XX 24-OCT-1997; 97US-0063120P.
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XX 28-OCT-1997; 97US-0063540P.
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XX 26-JUN-1998; 98US-0090863P.
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XX 01-JUL-1998; 98US-0091359P.
XX 01-JUL-1998; 98US-0091544P.
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Qy	61	VTIQEGGTIIVTQNRNRERVD	PDGGYSLKSLKKNDSGIYYVGIYSSSQPSTQEY	120
Db	61	VTIQEGGTIIVTQNRNRERVD	PDGGYSLKSLKKNDSGIYYVGIYSSSQPSTQEY	120
Qy	121	VLHYVEHLSPKVTMGLOSNKNGT	CVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL	180
Db	121	VLHYVEHLSPKVTMGLOSNKNGT	CVTNLTCCMEHGEEDVIYTWKALGOAANESHNGSIL	180
Qy	181	PISWRGESDMTFCVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSL	240	
Db	181	PISWRGESDMTFCVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSL	240	
Qy	241	FVLGLFWLFLKREQEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA	300	
Db	241	FVLGLFWLFLKREQEYIEKKRVDICRETPNICPHSGENTYDTIPTHTNRTILKEDPA	300	
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ID	ABU84358			
XX	ABU84358 standard; protein; 335 AA.			
AC	ABU84358;			
DT	02-AUG-2003 (first entry)			
DE	Human secreted/transmembrane protein (PRO) #96.			
XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;			
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;			
KW	tissue typing.			
XX	Homo sapiens.			
OS	US2003032112-A1.			
PN	13-FEB-2003.			
XX	21-JUN-2002; 2002US-00176756.			
XX	18-SEP-1997; 97US-0059263P.			
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Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

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PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096959P.
PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097955P.
PR	03-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
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PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101751P.
PR	10-JUN-1998;	98US-0088826P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100919P.
PR	11-JUN-1998;	98US-0088876P.	PR	18-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;				

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PR 02-OCT-1998; 98US-0102965P.
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PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYLWLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIIVTNTTPL 60
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Db 1 MAGSPTCLTLLIYLWLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIIVTNTTPL 60
   |||||

QY 61 VTIOPEGGTIIIVTQNNRERVDPDGGYSLKSLKNDGSIYVGIYSSSIQQPSTORY 120
   |||||
Db 61 VTIOPEGGTIIIVTQNNRERVDPDGGYSLKSLKNDGSIYVGIYSSSIQQPSTORY 120
   |||||

QY 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALQAAANESHNGSIL 180
   |||||
Db 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALQAAANESHNGSIL 180
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QY 181 PISWRGSDMTFICVARNPVSRNFPSSPILARKLCEGAADDPDSSMWLCLLLVPLLSL 240
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Db 181 PISWRGSDMTFICVARNPVSRNFPSSPILARKLCEGAADDPDSSMWLCLLLVPLLSL 240
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QY 241 FVLGLFLWFLKREOREYEEKKRVDICRETENICPHSGENTYDTIPIHTNRTILKEDPA 300
   |||||
Db 241 FVLGLFLWFLKREOREYEEKKRVDICRETENICPHSGENTYDTIPIHTNRTILKEDPA 300
   |||||

QY 301 NTVYSTVEIPKKOVNPHSLTTPDTPRLFAYENVI 335
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Db 301 NTVYSTVEIPKKOVNPHSLTTPDTPRLFAYENVI 335
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RESULT 12
ABR66232
ID ABR66232 standard; protein; 335 AA.
AC ABR66232;
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XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnerary; gene therapy.
XX
OS Homo sapiens.
XX
XX
PN US2003027278-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176987.
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PR 18-SEP-1997; 97US-0059263P.
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PR 21-OCT-1997; 97US-0063488P.
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PR 16-JUN-1998; 98US-0089514P.
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PR 17-SEP-1998;	98US-0100930P.		
PR 18-SEP-1998;	98US-0100849P.		
PR 18-SEP-1998;	98US-0101014P.		
PR 23-SEP-1998;	98US-0101068P.		
PR 23-SEP-1998;	98US-0101471P.		

Query Match

Best Local Similarity

Matches 335; Conservative

100.0%; Score 335; DB 6; Length 335;

Pred. No. 1.6e-314;

Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGSPTCLTLIYLWLTGSAASGPVKELVSGVGAVTFLKSKVKQVDSIVVTNTTTL	60
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Qy	61	VTIQPEGGTIIVTQNRNRVDFFDGGYSLKSLKXKNDSDGIYYVGIYSSSLQQPSTQY	120
Db	61	VTIQPEGGTIIVTQNRNRVDFFDGGYSLKSLKXKNDSDGIYYVGIYSSSLQQPSTQY	120
Qy	121	VLHYYEHLSPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQAANESHNGSL	180
Db	121	VLHYYEHLSPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQAANESHNGSL	180
Qy	181	PISWEGESDMTFFICVARNPVSRNFSSPILARKLCEGAADDDPSMVLCLLLVPLLSL	240
Db	181	PISWEGESDMTFFICVARNPVSRNFSSPILARKLCEGAADDDPSMVLCLLLVPLLSL	240
Qy	241	FVLGLFLWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPIHTNRTILKEDPA	300
Db	241	FVLGLFLWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPIHTNRTILKEDPA	300
Qy	301	NTVSTVEIPKKMENPHSLLTMPDTPRLFAYENVI	335
Db	301	NTVSTVEIPKKMENPHSLLTMPDTPRLFAYENVI	335

RESULT 13

ABR65622

ID ABR65622 standard; protein; 335 AA.

XX ABR65622;

XX ABR65622;

DT 05-AUG-2003 (first entry)

DE Human secreted polypeptide PRO1138, SEQ ID NO:192.

XX Human; PRO; secreted protein; transmembrane protein;

XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;

XX chondrocyte; proliferation; differentiation; cartilage disorder;

XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;

XX adrenal tumour; lung; colon; breast; prostate; kidney; cervix;

XX liver; drug screening; transgenic animal; genetic analysis;

XX antiarthritic; vulnery; gene therapy.

OS Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00188773.

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PR 15-SEP-1998; 98US-0100388P.
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PR 16-SEP-1998; 98US-0101933P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 23-SEP-1998; 98US-0101471P.
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PR 25-SEP-1998; 98US-0101786P.
PR 29-SEP-1998; 98US-0102207P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
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PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Query Match 100.0%; Score 335; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.6e-314;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYLWLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIVWTTNTPL 60
DB 1 MAGSPTCLTLLIYLWLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIVWTTNTPL 60
QY 61 VTIOPEGGTTIYTONNRRVDFPDGGYSLKLSKLKNDGSIYVGIYSSSIQQPSTORY 120
DB 61 VTIOPEGGTTIYTONNRRVDFPDGGYSLKLSKLKNDGSIYVGIYSSSIQQPSTORY 120
QY 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMERGEEDVIYTKALQAAANESHGSL 180
DB 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMERGEEDVIYTKALQAAANESHGSL 180
QY 181 PISRWGESDMTFICVARNPVSRNFSPTLARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
DB 181 PISRWGESDMTFICVARNPVSRNFSPTLARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKEROEYEEKKRVDICRETNI CPHSGENTYDTI PHTNRTILKEOPA 300
DB 241 FVLGLFLWFLKEROEYEEKKRVDICRETNI CPHSGENTYDTI PHTNRTILKEOPA 300
QY 301 NTVYSTVEIPKKMNPNSLLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKMNPNSLLTTPDTPRLPAYENVI 335
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RESULT 14
ABU99562
ID ABU99562 standard; protein; 335 AA.
XX AC ABU99562;
XX DT 09-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #96.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX OS Homo sapiens.
XX PN US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
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XX PR 05-MAY-1998; 98US-0084366P.
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Job time : 59 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:44:56 ; Search time 53 Seconds
(without alignments)
1785.913 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database :

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1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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146	1772	100.0	335	6	ABO09037	Human sec	219	1772	100.0	335	6	ABR93175	Human sec
147	1772	100.0	335	6	ABU96461	Human PRO	220	1772	100.0	335	6	ABR93480	Human sec
148	1772	100.0	335	6	ABU10885	Human PRO	221	1772	100.0	335	6	ADA10237	Human sec
149	1772	100.0	335	6	ABU10605	Human sec	222	1772	100.0	335	6	ABR87905	Human sec
150	1772	100.0	335	6	ABU81637	Novel hum	223	1772	100.0	335	6	ABO27905	Human sec
151	1772	100.0	335	6	ABU72131	Human PRO	224	1772	100.0	335	6	ABO30040	Human sec
152	1772	100.0	335	6	ABU95614	Human PRO	225	1772	100.0	335	6	ABO33249	Human PRO
153	1772	100.0	335	6	ABU96823	Novel hum	226	1772	100.0	335	6	ABM04937	Human sec
154	1772	100.0	335	6	ABR70668	Human sec	227	1772	100.0	335	6	ABM08897	Human sec
155	1772	100.0	335	6	ABO05019	Novel hum	228	1772	100.0	335	6	ABO36497	Human sec
156	1772	100.0	335	6	ABO08427	Human sec	229	1772	100.0	335	6	ABO35582	Human PRO
157	1772	100.0	335	6	ABU88576	Human sec	230	1772	100.0	335	6	ABO39547	Human sec
158	1772	100.0	335	6	ABO34090	Human PRO	231	1772	100.0	335	6	ABM10422	Human sec
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161	1772	100.0	335	6	ABR95615	Human sec	234	1772	100.0	335	6	ABO52398	Human PRO
162	1772	100.0	335	6	ABR80912	Human sec	235	1772	100.0	335	6	ADA19908	Novel hum
163	1772	100.0	335	6	ABR81217	Human sec	236	1772	100.0	335	6	ABO23716	Human sec
164	1772	100.0	335	6	ABM00913	Human sec	237	1772	100.0	335	6	ADB17291	Human tra
165	1772	100.0	335	6	ABR88515	Human sec	238	1772	100.0	335	6	ADA17781	Human PRO
166	1772	100.0	335	6	ABM77336	Human sec	239	1772	100.0	335	6	ABR97202	Human PRO
167	1772	100.0	335	6	ABO28820	Human sec	240	1772	100.0	335	6	ABR86990	Human sec
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169	1772	100.0	335	6	ABM07982	Human sec	242	1772	100.0	335	6	ABM28176	Human sec
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171	1772	100.0	335	6	ABO35887	Human PRO	244	1772	100.0	335	6	ABM15302	Human sec

245	1772	100.0	335	6	ABM06457	Human sec	318	1772	100.0	335	6	ABO28515	Human sec
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249	1772	100.0	335	6	ABO40767	Human sec	322	1772	100.0	335	6	ABO37107	Human sec
250	1772	100.0	335	6	ABM35414	Human sec	323	1772	100.0	335	6	ABO41682	Human sec
251	1772	100.0	335	6	ABM33177	Human sec	324	1772	100.0	335	6	ABO35277	Human PRO
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256	1772	100.0	335	6	ABO05939	Human sec	329	1772	100.0	335	6	ABO51483	Human PRO
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267	1772	100.0	335	6	ABM10117	Human sec	340	1772	100.0	335	6	ABM24211	Human sec
268	1772	100.0	335	6	ABO38632	Human sec	341	1772	100.0	335	6	ABM14632	Human sec
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273	1772	100.0	335	6	ABR96287	Human sec	346	1772	100.0	335	6	ABM75507	Human sec
274	1772	100.0	335	6	ABM02438	Human sec	347	1772	100.0	335	6	ABM25431	Human sec
275	1772	100.0	335	6	ABR86380	Human sec	348	1772	100.0	335	6	ABM19941	Human sec
276	1772	100.0	335	6	ABR86685	Human sec	349	1772	100.0	335	6	ABO46847	Human PRO
277	1772	100.0	335	6	ABM16649	Human sec	350	1772	100.0	335	6	ABO47152	Human PRO
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281	1772	100.0	335	6	ABM23296	Human sec	354	1772	100.0	335	6	ABR98532	Human sec
282	1772	100.0	335	6	ABM22076	Human sec	355	1772	100.0	335	6	ABO06902	Human sec
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522	1392.5	78.6	328	5	ABM33787	Human sec
523	933.5	52.7	684	4	ABM20246	Human sec
524	933.5	52.7	684	4	ABO48738	Human sec
525	622	35.1	124	2	ABO22546	Human sec
526	582	32.8	110	3	ABR72803	Human sec
527	582	32.8	110	3	ABO15445	Human sec
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529	582	32.8	110	6	ABO15140	Human sec
530	582	32.8	110	6	ABO17275	Human sec
531	582	32.8	110	6	ABM17564	Human sec
532	498	28.1	97	3	ADA06542	Human sec
533	498	28.1	98	2	ADA39235	Human sec
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535	471	26.6	91	4	ABM77031	Human sec
536	471	26.6	91	4	ABO28210	Human sec
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568	1772	100.0	335	7	ADC07002	Human PRO
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570	1772	100.0	335	7	ADC17181	Mammalian
571	1772	100.0	335	7	ADC07441	Human sec
572	1772	100.0	335	7	ADC11431	Human sec
573	1772	100.0	335	7	ADC14879	Novel hum
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537	471	26.6	91	4	ABB26408	Abb26408 Protein #	610	311	17.6	332	8	ADE77312	Ade77312 Human sec
538	471	26.6	91	4	AAM77190	Aam77190 Human bon	611	311	17.6	332	8	ADE65420	Ade65420 Human PRO
539	471	26.6	91	4	AAM64367	Aam64367 Human bra	612	311	17.6	332	8	ADE76029	Ade76029 Human PRO
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545	362.5	20.5	329	2	AAM74891	Aaw74891 Human nov	618	311	17.6	332	8	ADE38769	Ade38769 Human PRO
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548	343.3	19.4	629	5	AAM74424	Aau74424 Mouse pro	621	311	17.6	332	8	ADD90145	Add90145 Human sec
549	333.5	18.8	289	5	ADE26250	Aae26250 Human CD2	622	311	17.6	332	8	ADD90145	Add90145 Human sec
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566	313.5	17.7	331	5	AAE26240	Aae26240 Human CD2	639	225.5	12.7	351	4	ABM47322	Abm47322 Human pol
567	312.5	17.6	610	5	AAU74425	Aau74425 Human pro	640	209	12.4	168	5	ABH89245	Abh89245 Human pol
568	311.5	17.6	331	5	AAE26242	Aae26242 Human CD2	641	206	11.6	220	6	ABU03171	Abu03171 Human imm
569	311	17.6	332	4	AAE26242	Aae26242 Human CD2	642	200.5	11.3	159	5	AAE26225	Aae26225 Human CD2
570	311	17.6	332	5	ABG96267	Abg96267 Human imm	643	199.5	11.3	221	5	ABG96266	Abg96266 Human imm
571	311	17.6	332	5	ABG34067	Abg34067 Human pro	644	186	10.5	343	2	AAE26232	Aae26232 Mouse SLA
572	311	17.6	332	6	ABU03170	Abu03170 Human imm	645	182.5	10.3	335	2	AAE26232	Aae26232 Human SLA
573	311	17.6	332	6	ADA37159	Ada37159 Human PRO	646	182.5	10.3	335	2	AAE26232	Aae26232 Human SLA
574	311	17.6	332	6	ADA01344	Ada01344 Human PRO	647	182.5	10.3	335	5	AAU11927	Aau11927 Human tra
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577	311	17.6	332	6	ADA01216	Ada01216 Human PRO	650	181.5	10.2	334	5	ABG77978	Abg77978 Human sig
578	311	17.6	332	7	ADA01100	Ada01100 Human sec	651	180	10.2	307	2	AAE26231	Aae26231 Human SLA
579	311	17.6	332	7	ADA03657	Ada03657 Human sec	652	179	10.1	278	3	AAE26231	Aae26231 Human SLA
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581	311	17.6	332	7	ADA08407	Ada08407 Novel hum	654	179	10.1	278	7	ABW01426	Abw01426 Murine TA
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583	311	17.6	332	7	ADB86983	Adb86983 Human PRO	656	175	9.9	33	2	AAE26231	Aae26231 Fragment
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585	311	17.6	332	7	ADB99816	Adb99816 Human PRO	658	170	9.6	365	2	AAE26231	Aae26231 Human EST
586	311	17.6	332	7	ADB99471	Adb99471 Novel hum	659	170	9.6	365	5	AAU11929	Aau11929 Human pro
587	311	17.6	332	7	ADB66022	Adb66022 Human sec	660	170	9.6	391	5	ABP41447	Abp41447 Human ova
588	311	17.6	332	7	ADC23420	Adc23420 Human tra	661	164.5	9.3	305	2	AAE26231	Aae26231 Human SLA
589	311	17.6	332	7	ADC26113	Adc26113 Human PRO	662	164.5	9.3	305	5	ABE90777	AbE90777 Human Tum
590	311	17.6	332	7	ADE04940	Ade04940 Human PRO	663	164.5	9.3	305	6	ABU54484	Abu54484 Human nor
591	311	17.6	332	7	ADE11246	Ade11246 Human PRO	664	158.5	8.9	329	2	AAU11928	Aau11928 Mouse SLA
592	311	17.6	332	7	ADD88177	Add88177 Human PRO	665	158.5	8.9	329	5	AAU11928	Aau11928 Mouse pro
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594	311	17.6	332	7	ADE06402	Ade06402 Human PRO	667	152	8.6	298	6	ABE90778	AbE90778 Human Tum
595	311	17.6	332	7	ADE38177	Ade38177 Human PRO	668	152	8.6	298	6	ABU54485	Abu54485 Human nor
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597	311	17.6	332	7	ADD90874	Add90874 Human sec	670	150.5	8.5	285	4	AAE26231	Aae26231 Human pol
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599	311	17.6	332	8	ADE51843	Ade51843 Human sec	672	150.5	8.5	285	4	AAE26231	Aae26231 APEX-3 . 8
600	311	17.6	332	8	ADE37701	Ade37701 Human sec	673	150.5	8.5	285	4	AAE26231	Aae26231 Dendritic
601	311	17.6	332	8	ADE37585	Ade37585 Human sec	674	150.5	8.5	285	5	ABG32412	Abg32412 Dendritic
602	311	17.6	332	8	ADD95356	Add95356 Human sec	675	150.5	8.5	285	7	ADC78929	Adc78929 Human PRO
603	311	17.6	332	8	ADE52379	Ade52379 Human PRO	676	150.5	8.5	285	7	ADD18914	Add18914 Human dS
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607	311	17.6	332	8	ADE04272	Ade04272 Human PRO	680	146	8.2	312	7	ABW01412	Abw01412 Human TAN
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683 146 8.2 320 6 ABG74267 Human tra
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ALIGNMENTS

RESULT 1

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 ID AAY66701 standard; protein; 335 AA.

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DT 05-APR-2000 (first entry)

XX
 DE Membrane-bound protein PRO1138.

XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW Pharmaceutical; receptor immunoadhesin; gene mapping.

XX
 OS Homo sapiens.

XX
 PN WO9963088-A2.

XX
 PD 09-DEC-1999.

XX
 PF 02-JUN-1999; 99WO-US012252.

XX
 PR 02-JUN-1998; 98US-0087607P.

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PR 03-JUN-1998; 98US-0087827P.

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PR 05-JUN-1998; 98US-0088167P.

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 XX 02-MAR-2000.
 XX
 XX 24-AUG-1999; 99WO-US019386.
 XX
 XX 25-AUG-1998; 98US-00155261.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Lal P, Corley NC, Gorgone GA, Guegler KJ, Patterson C, Baughn MR;
 PI WPI; 2000-246561/21.
 DR N-PSDB; AA251572.
 DR
 XX New human cell surface immunomodulatory polypeptides and polynucleotides
 XX useful for diagnosis, prevention and treatment of cancer and immune
 XX disorders.
 XX
 XX Claim 1; Page 61-62; 70pp; English.
 XX
 XX The present sequence is the human cell surface immunomodulator-1 (CSIMM-
 CC 1), which is a regulator of cell proliferation, differentiation, cell-
 CC cell communication and signal transduction. It is encoded by cDNA
 CC identified in Incyte clone 14448, derived from human promonocyte cell
 CC line (THP-1) cDNA library (THP1PLB01). It shows homology to cell surface
 CC antigen, CD84. CSIMM can be used for drug screening, prevention and
 CC treatment of cancers such as leukaemia and melanoma, immune disorders
 CC such as AIDS, rheumatoid arthritis, asthma, atherosclerosis, diabetes
 CC mellitus, emphysema, irritable bowel syndrome, multiple sclerosis,
 CC osteoporosis, psoriasis and microbial infections. CSIMM polynucleotide
 CC may be used for diagnosis of CSIMM-associated diseases and as source of
 CC probes useful in mapping naturally occurring genomic sequences
 XX
 XX Sequence 335 AA;
 SQ
 Query Match 100.0%; Score 1772; DB 3; Length 335;
 Best Local Similarity 100.0%; Pred. No. 6.9e-163; Indels 0; Gaps 0;
 Matches 335; Conservative 0; Mismatches 0;
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 DB 1 MAGSPCTCLTLYLWLTGSAAGPVKELVGVGGAVTPPLKSKVQVDSIVTNTTPL 60
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 DB 61 VTIQPEGGTIIVTQNRNRVFPDGGYSLKLSKLKNDSDGIYVGYSSSLQQPSTQRY 120
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 DB 121 VLHVYELSKPKVTWGLQSNKNGTCVTNLTCCMEHGEDVIYTWKALGOARNESHNGSIL 180

QY 181 PISRWGESDMTFICVARNPVSRNFSPILARKLCEGAADPDSSMWLLCILLVPLLLSL 240
 DB 181 PISRWGESDMTFICVARNPVSRNFSPILARKLCEGAADPDSSMWLLCILLVPLLLSL 240
 QY 241 FVLGLFWLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
 DB 241 FVLGLFWLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
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 DB 301 NTVYSTVEIPKKNPHSLLTMPDTPRLFAVENVI 335
 RESULT 3
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 ID AAY44609 standard; protein; 335 AA.
 XX
 AC AAY44609;
 XX
 DT 07-APR-2000 (first entry)
 XX
 XX Human myocardium protein-7.
 DE Human myocardium protein-7.
 KW Human myocardium protein-7; MP-7; congestive heart failure;
 KW cardiovascular disorder; cardiomyopathy; hypertension; atherosclerosis;
 KW coronary artery spasm; coronary artery disease; cell-cell interaction;
 KW hypotensive; cardiant; screening assay.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..23
 FT /label= Signal_peptide
 FT Protein 24..335
 FT /note= "mature protein"
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 FT /note= "Second extracellular Ig-like domain"
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 FT /label= Leucine_zipper_domain
 FT Domain 250..335
 FT /label= Cytoplasmic_domain
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 WO9967387-A2.
 XX
 XX 29-DEC-1999.
 XX
 XX 24-JUN-1999; 99WO-US014307.
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 XX 25-JUN-1998; 98US-0090579P.
 PR 29-SEP-1998; 98US-00163284.
 PR 02-MAR-1999; 99US-00261759.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Khodadoust M;
 PI
 XX
 DR WPI; 2000-136984/12.
 DR N-PSDB; AA249571.
 XX
 PT Novel myocardium protein-7 polynucleotides, used to modulate a variety of
 FT cellular processes.
 XX
 XX Claim 2; Fig 2; 116pp; English.
 XX
 CC The present sequence is myocardium protein-7 (MP-7). MP-7 is used to
 CC modulate a variety of cellular processes e.g. modulating the activity of
 CC proteins involved in cardiovascular disorders like congestive heart
 CC failure or cardiomyopathy. Diseases which can be treated include
 CC hypertension, atherosclerosis, coronary artery spasm, and coronary artery

CC disease. MP-7 proteins may also be used for cellular regulation of immune
CC cell types, cell cycle, differentiation of multipotent cells, and
CC modulation of cell-cell interactions. MP-7 may also be used in screening
CC assays to identify agonists and antagonists and to raise antibodies
XX
SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 3; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAGSPCTCLTIYILWLTGSAASGPVKELVSGVGGAVTFPLKSKVKQVDSIVVTFNTTTL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGIYSSSQQPSTQY 120
DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGIYSSSQQPSTQY 120
QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSL 180
DB 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSL 180
QY 181 PISWRGSDMTFICVARNPVSRNFSPIARKLCEGAADDDPSSMVLCLLLVPLLSL 240
DB 181 PISWRGSDMTFICVARNPVSRNFSPIARKLCEGAADDDPSSMVLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKREQEYIEEKKRVDCIETPNICPHSGENTYDITPHNTNLTILKEDPA 300
DB 241 FVLGLFLWFLKREQEYIEEKKRVDCIETPNICPHSGENTYDITPHNTNLTILKEDPA 300
QY 301 NTVYSTVEIPKKNENPHSLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKNENPHSLTTPDTPRLPAYENVI 335

RESULT 4

AAU29119
ID AAU29119 standard; protein; 335 AA.
AC AAU29119;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #96.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS46020.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumors, such as prostate and breast tumors, in mammals and to
screen for modulators of the compounds.

Claim 11; Fig 192; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, rectal, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders

Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWLTGSAASGPVKELVSGVGGAVTFPLKSKVKQVDSIVVTFNTTTL 60
DB 1 MAGSPCTCLTIYILWLTGSAASGPVKELVSGVGGAVTFPLKSKVKQVDSIVVTFNTTTL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGIYSSSQQPSTQY 120
DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYVYGIYSSSQQPSTQY 120
QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSL 180

Db 121 VLHVYHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSL 180
Qy 181 PISWRGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLLVPLLSL 240
Db 181 PISWRGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLLVPLLSL 240
Qy 241 FVLGLFWFLKRRQEEYIEKKRVDICRETNPICPHSGENTYDTIPHTNRTILKEDPA 300
Db 241 FVLGLFWFLKRRQEEYIEKKRVDICRETNPICPHSGENTYDTIPHTNRTILKEDPA 300
Qy 301 NTVYSTVEIPKMPENPHSLTMDPTPRLFAYENVI 335
Db 301 NTVYSTVEIPKMPENPHSLTMDPTPRLFAYENVI 335

RESULT 5
AAB87548
ID AAB87548 standard; protein; 335 AA.

XX AAB87548;
XX 15-MAY-2001 (first entry)
XX Human PRO1138.
XX Human; PRO protein; mapping.
XX Homo sapiens.
XX WO200116318-A2.
XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-US023328.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 07-DEC-1999; 99US-0169495P.
XX 09-DEC-1999; 99US-0170262P.
XX 11-JAN-2000; 2000US-0175481P.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 22-FEB-2000; 2000WO-US004414.
XX 01-MAR-2000; 2000WO-US005601.
XX 03-MAR-2000; 2000WO-US0187202P.
XX 21-MAR-2000; 2000US-0191007P.
XX 30-MAR-2000; 2000WO-US008439.
XX 25-APR-2000; 2000US-0199397P.
XX 22-MAY-2000; 2000WO-US014042.
XX 05-JUN-2000; 2000US-0209832P.

XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX WPI; 2001-183260/18.
XX N-PSDB; AAF92080.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping.
XX Claim 12; Fig 46; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and
XX transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX anti-PRO antibodies are useful for preparation of a medicament useful in
XX the treatment of a condition which is responsive to the PRO protein,
XX agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX employed as molecular weight markers for protein electrophoresis. The PRO
XX coding sequence has applications in molecular biology, including use as
XX hybridisation probes, and in chromosome and gene mapping

XX Sequence 335 AA;
SQ Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163; Mismatches 0; Gaps 0;
Matches 335; Conservative 0;
Qy 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVWTFNTTPL 60
Qy 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKNDSDGIYVYVSSSQOQSTOEY 120
Db 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKNDSDGIYVYVSSSQOQSTOEY 120
Qy 121 VLHVYHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSL 180
Db 121 VLHVYHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALQQAANESHGSL 180
Qy 181 PISWRGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLLVPLLSL 240
Db 181 PISWRGSDMTFICVARNPVSRNFSPIILARKLCEGAADPDSSMVLCLLLVPLLSL 240
Qy 241 FVLGLFWFLKRRQEEYIEKKRVDICRETNPICPHSGENTYDTIPHTNRTILKEDPA 300
Db 241 FVLGLFWFLKRRQEEYIEKKRVDICRETNPICPHSGENTYDTIPHTNRTILKEDPA 300
Qy 301 NTVYSTVEIPKMPENPHSLTMDPTPRLFAYENVI 335
Db 301 NTVYSTVEIPKMPENPHSLTMDPTPRLFAYENVI 335

RESULT 6
AAB47321
ID AAB47321 standard; protein; 335 AA.
XX AC AAB47321;
XX 29-AUG-2001 (first entry)
XX APEX-1.

XX Antigen presenting cell expression protein; APEX-1; APEX-2; APEX-3;
XX extracellular domain; immunoglobulin-like domain; Ig-like structure;
XX N-glycosylation site; transmembrane domain; cytoplasmic domain;
XX SH2-binding motif; asthma; arteriosclerosis; AIDS; cirrhosis;
XX Crohn's disease; atopic dermatitis; autoimmune anaemia; bursitis;
XX cholecystitis; diabetes mellitus; emphysema; atrophic gastritis;
XX inflammatory bowel disease; multiple sclerosis; myasthenia gravis;
XX myocardial inflammation; pericardial inflammation; osteoarthritis;
XX osteoporosis; psoriasis; Reiter's syndrome; rheumatoid arthritis;
XX inflammation; cancer; autoimmune disease; graft rejection;
XX graft versus host disease; systemic lupus erythematosus.

XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..22
XX Protein /label= Signal peptide
XX 23..335
XX Domain /label= Mature APEX-1
XX 226..250
XX /label= Transmembrane domain

XX WO200146260-A2.
XX 28-JUN-2001.
XX 22-DEC-2000; 2000WO-US034963.
XX 23-DEC-1999; 99US-0172025P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Starling GC, Finger J;
PI WPI: 2001-418044/44.
DR N-PSDB; AAC86114.
XX
XX Novel Antigen presenting cell expression protein useful for treating
PT asthma, arteriosclerosis, autoimmune diseases, AIDS, cirrhosis, Crohn's
PT disease and atopic dermatitis.
XX
XX Claim 3; Fig 2; 112pp; English.
XX
XX The sequences given in AAB47321-23 represent antigen presenting cell
CC expression (APEX)-1, APEX-2 and APEX-3 proteins. APEX-1 and APEX-2
CC comprise an extracellular domain having one immunoglobulin (Ig)-like
CC structure and N-glycosylation site, a transmembrane domain, and a
CC cytoplasmic domain having at least one SH2-binding motif. APEX proteins
CC and antibodies are useful in the study, diagnosis, prevention and
CC treatment of disease associated with the presence of an APEX protein
CC e.g., asthma, arteriosclerosis, AIDS, cirrhosis, Crohn's disease, atopic
CC dermatitis, autoimmune anaemia, bursitis, cholecystitis, diabetes
CC mellitus, emphysema, atrophic gastritis, inflammatory bowel disease,
CC multiple sclerosis, myasthenia gravis, myocardial or pericardial
CC inflammation, osteoarthritis, osteoporosis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, inflammation, cancer, immune disorders, autoimmune
CC diseases, graft rejections, graft versus host reaction and systemic lupus
CC erythematosus. APEX proteins are useful as diagnostic and/or prognostic
CC markers on APCs or APEX expressing cells, the ability to elicit the
CC generation of antibodies and as targets for various therapeutic
CC modalities. APEX proteins are also useful for identifying and isolating
CC ligand that bind APEX
XX
XX Sequence 335 AA;
Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAGSPCTCLTIYILWLTGSAAGPVKELVGSVGGAVTFLKSKVKQVDSIVWTFNTPL 60
Db 1 MAGSPCTCLTIYILWLTGSAAGPVKELVGSVGGAVTFLKSKVKQVDSIVWTFNTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDPFDGGYSLKSLKLNKDSGIYVVGIIYSSSLQQPSTQSY 120
Db 61 VTIOPEGGTIIVTQNRNRVDPFDGGYSLKSLKLNKDSGIYVVGIIYSSSLQQPSTQSY 120
QY 121 VLHVEHLKPKVTMGLOSKNGTCTVNLTCCEHGEEDVIYTWKALGOANESHNGSIL 180
Db 121 VLHVEHLKPKVTMGLOSKNGTCTVNLTCCEHGEEDVIYTWKALGOANESHNGSIL 180
QY 181 PISWRGESDWTFCVARNPVSRNFSFPIARLCEGAADDPSSMVLCLLIVPLLSSL 240
Db 181 PISWRGESDWTFCVARNPVSRNFSFPIARLCEGAADDPSSMVLCLLIVPLLSSL 240
QY 241 FVLGLFLWFLKREBEYIEKKRVDCRETNPICPHSGENTYDTPHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREBEYIEKKRVDCRETNPICPHSGENTYDTPHTNRTILKEDPA 300
QY 301 NTVYSTVEIPKQENPHSLTMDPTPLFAYENVI 335
Db 301 NTVYSTVEIPKQENPHSLTMDPTPLFAYENVI 335
RESULT 7
AAB65224
ID AAB65224 standard; protein; 335 AA.
XX
AC AAB65224;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1138 (UNQ576) protein sequence SEQ ID NO:253.
XX

KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX Homo sapiens.
XX OS
XX WO200073454-A1.
XX PD 07-DEC-2000.
XX
XX 30-MAR-2000; 2000WO-US008439.
XX
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149398P.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 08-OCT-1999; 99US-0158663P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 24-FEB-2000; 2000WO-US005004.
XX 02-MAR-2000; 2000WO-US005841.
XX 15-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX WPI: 2001-032160/04.
XX N-PSDB; AAF44186.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
XX Claim 12; Fig 171; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF4470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
XX Sequence 335 AA;
Query Match 100.0%; Score 1772; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYLTWLTGSAAGPVKELVGVSGGAVTFLKSKVKQVDSIVWTNTTTL 60
DB 1 MAGSPCTCLTIYLTWLTGSAAGPVKELVGVSGGAVTFLKSKVKQVDSIVWTNTTTL 60

QY 61 VTIQEGGTIIYVQNRNRVDFPDGGYSLKSLKKNDSGIYVYGVYSSSIQQPSTQY 120
DB 61 VTIQEGGTIIYVQNRNRVDFPDGGYSLKSLKKNDSGIYVYGVYSSSIQQPSTQY 120

QY 121 VLHVYHLKPKVTMGLQNKGTCTVNTLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180
DB 121 VLHVYHLKPKVTMGLQNKGTCTVNTLTCMEHGEEDVIYTWKALGOAANESHNGSIL 180

QY 181 PISWRGSDMTFICVARNPVRNFPSSPILARKLCEGAADDPDSSVLLCLLLVPLL 240
DB 181 PISWRGSDMTFICVARNPVRNFPSSPILARKLCEGAADDPDSSVLLCLLLVPLL 240

QY 241 FVLGLFLWFLKREQEYIEKKRVDICRETNPICPHSGENTYDTIPTHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREQEYIEKKRVDICRETNPICPHSGENTYDTIPTHTNRTILKEDPA 300

QY 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335
DB 301 NTVYSTVEIPKKNPHSLTTPDTPRLPAYENVI 335

RESULT 8
ABG95873
ID ABG95873 standard; protein; 335 AA.
AC ABG95873;
DT 10-DEC-2002 (first entry)
XX Human secreted/transmembrane protein PRO1138.
DE Human; secreted protein; transmembrane protein; antirheumatic;
KW antirheumatic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX Homo sapiens.

OS US2002119130-A1.
XX 29-AUG-2002.
XX 06-DEC-2001; 2001US-00006867.
XX 29-OCT-1997; 97US-0063435P.
XX 29-OCT-1997; 97US-0064215P.
XX 22-APR-1998; 98US-0082797P.
XX 29-APR-1998; 98US-0083495P.
XX 15-MAY-1998; 98US-0085579P.
XX 02-JUN-1998; 98US-0087759P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088740P.
XX 10-JUN-1998; 98US-0088811P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088825P.
XX 11-JUN-1998; 98US-0088863P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089653P.
XX 19-JUN-1998; 98US-0089952P.
XX 22-JUN-1998; 98US-0090246P.
XX 24-JUN-1998; 98US-0090444P.
XX 25-JUN-1998; 98US-0090688P.
XX 25-JUN-1998; 98US-0090698P.
XX 26-JUN-1998; 98US-0090862P.

PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 17-SEP-1998; 98US-0101279P.
PR 22-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015284.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
N-PSDB; ABS74400.

New isolated secreted and transmembrane PRO polypeptide useful for
modulating biological activity of a cell, or for treating sports-related
joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 46; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
polypeptide having 80 % sequence identity to a sequence appearing as
ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
extracellular domain of the proteins with their associated signal peptide
or lacking its associated signal peptide. Also included are the nucleic

CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 335 AA;

Query Match 100.0%; Score 1772; DB 5; Length 335;
 Best Local Similarity 100.0%; Pred. No. 6.9e-163;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MAGSPTCLTIYILWLTGSAAGPVKELVGSVGGAVTFLKSKVKQVDSIVWTFNTTTL 60
 QY 61 VTIQPEGGTIIYQNRNRVDPDGGYSILKSLKKNDSGIYVGIYSSSLQQPSTQBY 120
 Db 61 VTIQPEGGTIIYQNRNRVDPDGGYSILKSLKKNDSGIYVGIYSSSLQQPSTQBY 120
 QY 121 VLHVYHLKPKVTWGLQNKNGTCVNTLTCMEHGEEDVIYTWKALGOAANESHNGSTL 180
 Db 121 VLHVYHLKPKVTWGLQNKNGTCVNTLTCMEHGEEDVIYTWKALGOAANESHNGSTL 180
 QY 181 PISWRNGESDMTIFICVARNPVSNFSSPIARLKLCEGAADDPDSSNVLLCLLIVPLLLSL 240
 Db 181 PISWRNGESDMTIFICVARNPVSNFSSPIARLKLCEGAADDPDSSNVLLCLLIVPLLLSL 240
 QY 241 FVLGLFWLFLKRRQBEYIEEKRVDI CRETPNCPHSGENTYDTPHTNRTLKEDPA 300
 Db 241 FVLGLFWLFLKRRQBEYIEEKRVDI CRETPNCPHSGENTYDTPHTNRTLKEDPA 300
 QY 301 NTVYSTVEIPKKNPHSLLTWPDTPRLPAYENVI 335
 Db 301 NTVYSTVEIPKKNPHSLLTWPDTPRLPAYENVI 335

RESULT 9
 ABU58495

ID ABU58495 standard; protein; 335 AA.

XX

AC ABU58495;

XX DT 15-APR-2003 (first entry)
 XX DE Human PRO polypeptide #96.
 XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
 KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
 KW antibody-dependent enzyme mediated prodrug therapy.
 XX OS Homo sapiens.
 XX US2003027272-A1.
 XX PD 06-FEB-2003.
 XX PF 21-JUN-2002; 2002US-00176492.
 XX PR 18-SEP-1997; 97US-0059263P.
 PR 18-SEP-1997; 97US-0059266P.
 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 28-OCT-1997; 97US-0063540P.
 PR 28-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 24-NOV-1997; 97US-0066466P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 11-DEC-1997; 97US-0069335P.
 PR 12-DEC-1997; 97US-0069425P.
 PR 17-DEC-1997; 97US-0069870P.
 PR 18-DEC-1997; 97US-0068017P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078939P.
 PR 27-MAR-1998; 98US-0079664P.
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 PR 31-MAR-1998; 98US-0080107P.
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 PR 01-APR-1998; 98US-0080327P.
 PR 01-APR-1998; 98US-0080333P.
 PR 08-APR-1998; 98US-0081049P.
 PR 08-APR-1998; 98US-0081070P.
 PR 09-APR-1998; 98US-0081195P.
 PR 15-APR-1998; 98US-0081838P.
 PR 21-APR-1998; 98US-0082568P.
 PR 21-APR-1998; 98US-0082569P.
 PR 22-APR-1998; 98US-0082704P.
 PR 22-APR-1998; 98US-0082797P.
 PR 28-APR-1998; 98US-0083322P.
 PR 29-APR-1998; 98US-0083495P.
 PR 29-APR-1998; 98US-0083496P.
 PR 29-APR-1998; 98US-0083499P.
 PR 29-APR-1998; 98US-0083559P.
 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
 PR 07-MAY-1998; 98US-0084639P.
 PR 07-MAY-1998; 98US-0084640P.
 PR 07-MAY-1998; 98US-0084643P.
 PR 15-MAY-1998; 98US-0085579P.
 PR 15-MAY-1998; 98US-0085580P.
 PR 15-MAY-1998; 98US-0085582P.
 PR 15-MAY-1998; 98US-0085700P.
 PR 18-MAY-1998; 98US-0086023P.
 PR 22-MAY-1998; 98US-0086392P.

PR	22-MAY-1998	98US-0086486P.	PR	18-AUG-1998	98US-0097022P.	Query Match	100.0%;	Score 1772;	DB 6;	Length 335;
PR	28-MAY-1998	98US-0087098P.	PR	26-AUG-1998	98US-0097952P.	Best Local Similarity	100.0%;	Pred. No. 6.9e-163;		
PR	28-MAY-1998	98US-0087208P.	PR	26-AUG-1998	98US-0097954P.	Matches 335;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
PR	02-JUN-1998	98US-0087609P.	PR	26-AUG-1998	98US-0097955P.					
PR	02-JUN-1998	98US-0087759P.	PR	26-AUG-1998	98US-0097971P.	Qy	1	MAGSPCTLTIYILMOLTGSAASGPVKELVSGVAVFPPLKSKVKQVDSI	VWTTNTTPL	60
PR	03-JUN-1998	98US-0087827P.	PR	26-AUG-1998	98US-0097974P.	Db	1	MAGSPCTLTIYILMOLTGSAASGPVKELVSGVAVFPPLKSKVKQVDSI	VWTTNTTPL	60
PR	04-JUN-1998	98US-0088025P.	PR	26-AUG-1998	98US-0098014P.					
PR	04-JUN-1998	98US-0088028P.	PR	01-SEP-1998	98US-0098716P.	Qy	61	VTIQPEGGTIIIVTQNNRERVD	PDGGYSLKLSKLKNDSGIIYVVGIIYSSSLQQPSTQEQY	120
PR	04-JUN-1998	98US-0088029P.	PR	01-SEP-1998	98US-0098723P.	Db	61	VTIQPEGGTIIIVTQNNRERVD	PDGGYSLKLSKLKNDSGIIYVVGIIYSSSLQQPSTQEQY	120
PR	04-JUN-1998	98US-0088033P.	PR	02-SEP-1998	98US-0098803P.					
PR	04-JUN-1998	98US-0088326P.	PR	02-SEP-1998	98US-0098821P.	Qy	121	VLHVYEHLSKPKVTMTGLQSNKNGTCTVNTLTCOMEHGEDVIYTWKALQAAANESHG	SIL	180
PR	05-JUN-1998	98US-0088167P.	PR	02-SEP-1998	98US-0098843P.	Db	121	VLHVYEHLSKPKVTMTGLQSNKNGTCTVNTLTCOMEHGEDVIYTWKALQAAANESHG	SIL	180
PR	05-JUN-1998	98US-0088212P.	PR	09-SEP-1998	98US-0099602P.					
PR	05-JUN-1998	98US-0088217P.	PR	10-SEP-1998	98US-0099741P.	Qy	181	PISWRWGESDMTFCIVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL		240
PR	09-JUN-1998	98US-0088655P.	PR	10-SEP-1998	98US-0099754P.	Db	181	PISWRWGESDMTFCIVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL		240
PR	10-JUN-1998	98US-0088722P.	PR	10-SEP-1998	98US-0099812P.					
PR	10-JUN-1998	98US-0088738P.	PR	15-SEP-1998	98US-0100388P.	Qy	181	PISWRWGESDMTFCIVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL		240
PR	10-JUN-1998	98US-0088811P.	PR	16-SEP-1998	98US-0100662P.	Db	181	PISWRWGESDMTFCIVARNPVSRNFSSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL		240
PR	10-JUN-1998	98US-0088824P.	PR	16-SEP-1998	98US-0100664P.					
PR	10-JUN-1998	98US-0088825P.	PR	16-SEP-1998	98US-0101751P.	Qy	241	FVLGLFWLKRERQEEYIEKKRVDICRETENICPHSGENTYDTIPTHTNRTILKEDPA		300
PR	10-JUN-1998	98US-0088826P.	PR	17-SEP-1998	98US-0100683P.					
PR	11-JUN-1998	98US-0088861P.	PR	17-SEP-1998	98US-0100684P.					
PR	11-JUN-1998	98US-0088863P.	PR	17-SEP-1998	98US-0100919P.					
PR	11-JUN-1998	98US-0088876P.	PR	17-SEP-1998	98US-0100930P.					
PR	12-JUN-1998	98US-0089090P.	PR	18-SEP-1998	98US-0100849P.					
PR	12-JUN-1998	98US-0089105P.	PR	18-SEP-1998	98US-0101014P.					
PR	16-JUN-1998	98US-0089512P.	PR	18-SEP-1998	98US-0101068P.					
PR	16-JUN-1998	98US-0089514P.	PR	23-SEP-1998	98US-0101471P.					
PR	17-JUN-1998	98US-0089598P.	PR	23-SEP-1998	98US-0101472P.					
PR	17-JUN-1998	98US-0089533P.	PR	23-SEP-1998	98US-0101475P.					
PR	18-JUN-1998	98US-0089508P.	PR	23-SEP-1998	98US-0101477P.					
PR	18-JUN-1998	98US-0089508P.	PR	24-SEP-1998	98US-0101738P.					
PR	19-JUN-1998	98US-0089552P.	PR	24-SEP-1998	98US-0101739P.					
PR	22-JUN-1998	98US-0090246P.	PR	24-SEP-1998	98US-0101743P.					
PR	22-JUN-1998	98US-0090252P.	PR	24-SEP-1998	98US-0101922P.					
PR	22-JUN-1998	98US-0090254P.	PR	25-SEP-1998	98US-0101786P.					

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR	02-JUL-1998;	98US-0091486P.
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PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096766P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100864P.
PR	16-SEP-1998;	98US-0101751P.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
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PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	25-SEP-1998;	98US-0102207P.
PR	25-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	05-OCT-1998;	98US-0103258P.

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGSPCTLIYILWLTGSAAGPKVLGVGGAVTFPLKSKVKQVDSIWTNTTFL	60
Db	1	MAGSPCTLIYILWLTGSAAGPKVLGVGGAVTFPLKSKVKQVDSIWTNTTFL	60

PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690B.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	25-JUN-1998;	98US-0090695P.
PR	09-APR-1998;	98US-0081070P.	PR	26-JUN-1998;	98US-0090696P.
PR	15-APR-1998;	98US-0081195P.	PR	26-JUN-1998;	98US-00105413.
PR	21-APR-1998;	98US-0081838P.	PR	26-JUN-1998;	98US-0090862P.
PR	21-APR-1998;	98US-0082568P.	PR	26-JUN-1998;	98US-0090863P.
PR	22-APR-1998;	98US-0082569P.	PR	26-JUN-1998;	98US-0090863P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091010P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-0091359P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-0091478P.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0091486P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0091544P.
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PR	05-MAY-1998;	98US-0084366P.	PR	02-JUL-1998;	98US-0091632P.
PR	06-MAY-1998;	98US-0084414P.	PR	24-JUL-1998;	98US-0094006P.
PR	07-MAY-1998;	98US-0084639P.	PR	04-AUG-1998;	98US-0095282P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-0095998P.
PR	07-MAY-1998;	98US-0084643P.	PR	10-AUG-1998;	98US-0096012P.
PR	15-MAY-1998;	98US-0085579P.	PR	17-AUG-1998;	98US-0096757P.
PR	15-MAY-1998;	98US-0085580P.	PR	17-AUG-1998;	98US-0096766P.
PR	15-MAY-1998;	98US-0085582P.	PR	17-AUG-1998;	98US-0096867P.
PR	18-MAY-1998;	98US-0085700P.	PR	17-AUG-1998;	98US-0096891P.
PR	22-MAY-1998;	98US-0086023P.	PR	17-AUG-1998;	98US-0096897P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0096959P.
PR	28-MAY-1998;	98US-0087098P.	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097552P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097955P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097971P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088028P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088033P.	PR	01-SEP-1998;	98US-0098723P.
PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098803P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088202P.	PR	02-SEP-1998;	98US-0098843P.
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PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088738P.	PR	10-SEP-1998;	98US-0099812P.
PR	10-JUN-1998;	98US-0088740P.	PR	15-SEP-1998;	98US-0100388P.
PR	10-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100662P.
PR	10-JUN-1998;	98US-0088824P.	PR	16-SEP-1998;	98US-0100664P.
PR	10-JUN-1998;	98US-0088825P.	PR	16-SEP-1998;	98US-0101753P.
PR	10-JUN-1998;	98US-0088826P.	PR	16-SEP-1998;	98WO-US019330.
PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100683P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-0100684P.
PR	11-JUN-1998;	98US-0088976P.	PR	17-SEP-1998;	98US-0100919P.
PR	12-JUN-1998;	9			

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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-00168978.

Query Match 100.0%; Score 1772; DB 6; Length 335;
Best Local Similarity 100.0%; Pred. No. 6.9e-163;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTIYILWOLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIWTNTTPL 60
DQ 1 MAGSPTCLTIYILWOLTGSAAGPVKELVSGVGAATPPLKSKVKQVDSIWTNTTPL 60
QY 61 VTIOPEGGIIIVTONRNRVDFPDGGYSLKSLKNDGSIYVYVYSSSLOQPSTORY 120
DQ 61 VTIOPEGGIIIVTONRNRVDFPDGGYSLKSLKNDGSIYVYVYSSSLOQPSTORY 120
QY 121 VLHVYHLKPKVTMGLQNKNGTCVTNLTCCMEHGEEDVIYTKALQOANESHNGSIL 180
DQ 121 VLHVYHLKPKVTMGLQNKNGTCVTNLTCCMEHGEEDVIYTKALQOANESHNGSIL 180
QY 181 PISWRGSDMTFICVARNPVSRNFSPIARLCEGAADDPDSSNVLLCLLLVPLLSL 240
DQ 181 PISWRGSDMTFICVARNPVSRNFSPIARLCEGAADDPDSSNVLLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKREOREYEIEEKRVVDICRETENICPHSGENTEXTDITPHNTIILKEDPA 300
DQ 241 FVLGLFLWFLKREOREYEIEEKRVVDICRETENICPHSGENTEXTDITPHNTIILKEDPA 300
QY 301 NTVYSTVEIPKQKMPHSLTTPDTPRLPAYENVI 335
DQ 301 NTVYSTVEIPKQKMPHSLTTPDTPRLPAYENVI 335

RESULT 12
ABR66232
ID ABR66232 standard; protein; 335 AA.
AC ABR66232;
XX
XX 05-AUG-2003 (first entry)
XX Human secreted polypeptide PRO1138, SEQ ID NO:192.
XX Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnery; gene therapy.
XX Homo sapiens.
XX
XX US2003027278-A1.
XX
XX 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-00176987.
XX
XX 18-SEP-1997; 97US-0059263P.
XX 18-SEP-1997; 97US-0059266P.
XX 17-OCT-1997; 97US-0062250P.
XX 21-OCT-1997; 97US-0063486P.
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Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VTIOPEGGTIIVTQNRNRERVDPPGGYSLKLSKLKNDGIIYVGIYSSSIQQPSTQY 120

Qy 121 VLHYVEHLSKPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSL 180
Db 121 VLHYVEHLSKPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSL 180

Qy 181 PISRWGESDMTFICVARNPVSRNPFSSPILARKLCEGAADDDPSNVLLCLLLVPLL 240
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Qy 241 FVLGLFLWFLKREOEYIEKKRYDICTETPNICPHSGENTYDTIHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREOEYIEKKRYDICTETPNICPHSGENTYDTIHTNRTILKEDPA 300

Qy 301 NTVYSTVEIPKXMPHSLTMTPTPRLFAVENVI 335
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RESULT 13
ABR65622
ID ABR65622 standard; protein; 335 AA.
XX
AC ABR65622;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1138, SEQ ID NO:192.
XX
KW Human; PRO; secreted protein; transmembrane protein; TNF-alpha;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036159-A1.
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PD 20-FEB-2003.
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PF 02-JUL-2002; 2002US-00188773.
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QY 181 PISWRGSDMTFICVARNPVSRNFSPIARLKLCEGAADDDPSSMVLCLLLVPLLSSL 240
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QY 301 NTVYSTVEIPKKMENPHSLLTMPDTPRLPAYENVI 335
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RESULT 14
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AC ABU99562;
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DT 09-AUG-2003 (first entry)
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DE Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
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XX OS Homo sapiens.
XX US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
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XX DT 14-APR-2003 (first entry)
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XX DE Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADAPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027163-A1.
XX PD 06-FEB-2003.
XX PF 15-NOV-2001; 2001US-00997666.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:56:34 ; Search time 39 Seconds
(without alignments)
2710.220 Million cell updates/sec

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Perfect score: 335

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Searched: 1017041 seqs, 315518202 residues

Word size : 0

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9: sp_phase.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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92	7	2.1	191	12	Q9J4B8	Q9j4b8 baboon cyto	165	7	2.1	336	10	Q7XVK0	Q7xvk0 oryza sativ
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94	7	2.1	195	15	Q7ZH61	Q7zh61 human immun	167	7	2.1	341	12	Q8JTX8	Q8jtx8 lumpy skin
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98	7	2.1	195	15	Q7ZH52	Q7zh52 human immun	171	7	2.1	344	8	Q8HIV9	Q8hiv9 bubo ascala
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104	7	2.1	204	12	Q66087	Q66087 canine herp	177	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
105	7	2.1	210	3	Q9UW23	Q9uw23 candida alb	178	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
106	7	2.1	212	8	Q8LWU5	Q8lwu5 gymnogobius	179	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
107	7	2.1	212	8	Q8LWV0	Q8lwk7 gymnogobius	180	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
108	7	2.1	212	8	Q8LWV1	Q8lwk7 gymnogobius	181	7	2.1	347	8	Q8HIV6	Q8hiv6 bubo bubo (
109	7	2.1	212	8	Q8LWV2	Q8lwk7 gymnogobius	182	7	2.1	348	17	Q9HPV6	Q9hnpv6 halobacteri
110	7	2.1	212	8	Q8LWV3	Q8lwk7 gymnogobius	183	7	2.1	349	16	Q9N1V7	Q9n1v7 rhizobium l
111	7	2.1	212	8	Q8LWV4	Q8lwk7 gymnogobius	184	7	2.1	351	16	Q9PF30	Q9pf30 xyella fae
112	7	2.1	212	8	Q8LWV5	Q8lwk7 gymnogobius	185	7	2.1	351	16	Q9PF30	Q9pf30 xyella fae
113	7	2.1	212	8	Q8LWV6	Q8lwk7 gymnogobius	186	7	2.1	353	16	Q87AJ8	Q87aj8 xyella fae
114	7	2.1	212	8	Q8LWV7	Q8lwk7 gymnogobius	187	7	2.1	356	8	Q8PF66	Q8pfs6 xanthomonas
115	7	2.1	212	8	Q8LWV8	Q8lwk7 gymnogobius	188	7	2.1	356	8	Q8PF66	Q8pfs6 xanthomonas
116	7	2.1	212	8	Q8LWV9	Q8lwk7 gymnogobius	189	7	2.1	360	11	Q8VIF0	Q8vif0 bubo virgin
117	7	2.1	215	9	Q8W6N4	Q8w6n4 bacterioph	190	7	2.1	360	11	Q8VIF0	Q8vif0 bubo virgin
118	7	2.1	215	9	Q8W6N4	Q8w6n4 bacterioph	191	7	2.1	364	5	Q9VBF5	Q9vbf5 drosophila
119	7	2.1	216	10	Q8E254	Q8e254 leptospira	192	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
120	7	2.1	220	16	Q8R220	Q8r220 rheinococcus	193	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
121	7	2.1	221	12	Q7TF2	Q7tf22 rheinococcus	194	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
122	7	2.1	224	2	Q9JNK7	Q9jnk7 yersinia en	195	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
123	7	2.1	224	2	Q9JNK7	Q9jnk7 yersinia en	196	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
124	7	2.1	224	2	Q9JNK7	Q9jnk7 yersinia en	197	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
125	7	2.1	226	16	Q8N2L3	Q8n2l3 streptococc	198	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
126	7	2.1	226	16	Q8N2L3	Q8n2l3 streptococc	199	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
127	7	2.1	226	16	Q8N2L3	Q8n2l3 streptococc	200	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
128	7	2.1	226	16	Q8N2L3	Q8n2l3 streptococc	201	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
129	7	2.1	238	16	Q9P032	Q9p032 bacillus su	202	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
130	7	2.1	238	16	Q9P032	Q9p032 bacillus su	203	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
131	7	2.1	238	16	Q9P032	Q9p032 bacillus su	204	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
132	7	2.1	244	8	Q3S892	Q3s892 squatina ne	205	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
133	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	206	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
134	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	207	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
135	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	208	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
136	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	209	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
137	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	210	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
138	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	211	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
139	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	212	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
140	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	213	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
141	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	214	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
142	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	215	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
143	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	216	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
144	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	217	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
145	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	218	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
146	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	219	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
147	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	220	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
148	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	221	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
149	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	222	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
150	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	223	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
151	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	224	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
152	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	225	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
153	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	226	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
154	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	227	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
155	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	228	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
156	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	229	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
157	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	230	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
158	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	231	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
159	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	232	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
160	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	233	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
161	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	234	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas
162	7	2.1	246	10	Q8L655	Q8l655 oryza sativ	235	7	2.1	367	16	Q88Q33	Q88qg3 pseudomonas

236	7	2.1	469	16	Q81NB5	Q81nb5 bacillus an	309	7	2.1	797	3	Q9UTK6	Q9utk6 schizosacch
237	7	2.1	469	16	Q81F82	Q81f82 bacillus ce	310	7	2.1	801	5	Q81FG4	Q81fg4 trypanosoma
238	7	2.1	470	5	Q9N4J9	Q9n4j9 caenorhabdi	311	7	2.1	803	10	Q9LWV8	Q9lww8 oryza sativ
239	7	2.1	470	5	Q9M3D9	Q9m3d9 arabidopsis	312	7	2.1	814	10	Q8S808	Q8s808 oryza sativ
240	7	2.1	480	16	Q8UG85	Q8ug85 agrobacteri	313	7	2.1	847	6	Q95KP7	Q95kp7 canis famil
241	7	2.1	487	5	Q9VZ97	Q9vz97 drosophila	314	7	2.1	870	4	Q8N639	Q8n639 homo sapien
242	7	2.1	492	16	Q9A4F0	Q9a4f0 caulobacter	315	7	2.1	870	4	Q7Z3F1	Q7z3f1 homo sapien
243	7	2.1	493	10	Q9AXF0	Q9axf0 oryza sativ	316	7	2.1	878	3	Q9USU3	Q9usu3 schizosacch
244	7	2.1	496	5	Q961I9	Q961i9 drosophila	317	7	2.1	882	4	Q9V438	Q9v438 homo sapien
245	7	2.1	496	5	Q9VX74	Q9vx74 drosophila	318	7	2.1	946	5	O44825	O44825 caenorhabdi
246	7	2.1	500	10	Q8LKG1	Q8lkg1 mesembryant	319	7	2.1	946	16	Q827G6	Q827g6 streptomyc
247	7	2.1	501	4	Q9BU25	Q9bu25 homo sapien	320	7	2.1	947	5	Q8BIA3	Q8bia3 caenorhabdi
248	7	2.1	501	16	Q92X18	Q92x18 rhizobium m	321	7	2.1	951	5	Q8MUT5	Q8mut5 helicoverpa
249	7	2.1	504	6	Q95LK5	Q95lk5 macaca fasc	322	7	2.1	951	5	Q8MU79	Q8mu79 helicoverpa
250	7	2.1	505	5	Q8IM14	Q8im14 drosophila	323	7	2.1	951	5	Q86QI6	Q86qi6 helicoverpa
251	7	2.1	505	13	Q8JG64	Q8jg64 gallus gall	324	7	2.1	951	5	Q7Z268	Q7z268 helicoverpa
252	7	2.1	507	11	Q8VIF1	Q8vif1 rattus norv	325	7	2.1	957	16	Q83QA2	Q83qa2 shigella fl
253	7	2.1	509	5	Q8LQ93	Q8lq93 drosophila	326	7	2.1	959	16	Q7U3Q5	Q7u3q5 synechococc
254	7	2.1	513	11	Q8K052	Q8k052 mus musculu	327	7	2.1	963	11	Q8BX19	Q8bx19 mus musculu
255	7	2.1	513	17	Q9HMS7	Q9hms7 halobacteri	328	7	2.1	964	16	Q7V9K4	Q7v9k4 prochloroco
256	7	2.1	514	3	Q872D0	Q872d0 neurospora	329	7	2.1	965	2	Q9RA59	Q9ra59 thermus cal
257	7	2.1	517	2	Q8KY45	Q8ky45 streptomyc	330	7	2.1	965	2	Q7WUI5	Q7wu15 thermus the
258	7	2.1	518	10	Q7Y0V8	Q7y0v8 oryza sativ	331	7	2.1	969	16	Q7WR47	Q7wr47 bordetella
259	7	2.1	522	16	Q8NP67	Q8np67 corynebacte	332	7	2.1	969	16	Q7UZJ5	Q7uzj5 prochloroco
260	7	2.1	524	12	Q86404	Q86404 rabies viru	333	7	2.1	977	5	Q8WRU7	Q8wru7 trypanosoma
261	7	2.1	524	12	Q8DKD1	Q8dkd1 rabies viru	334	7	2.1	1019	11	Q8BJQ7	Q8bjq7 mus musculu
262	7	2.1	524	12	Q86393	Q86393 rabies viru	335	7	2.1	1031	6	Q8HZ52	Q8hz52 felis silve
263	7	2.1	524	12	Q86385	Q86385 rabies viru	336	7	2.1	1057	5	Q8MR83	Q8mr83 drosophila
264	7	2.1	532	5	Q9VCQ0	Q9vcq0 drosophila	337	7	2.1	1057	5	Q869U6	Q869u6 dictyosteli
265	7	2.1	532	5	Q94CQ5	Q94cq5 oryza sativ	338	7	2.1	1070	10	Q9SV36	Q9sv36 arabidopsis
266	7	2.1	532	11	Q99J23	Q99j23 mus musculu	339	7	2.1	1133	5	Q8MKU4	Q8mku4 drosophila
267	7	2.1	532	11	Q99J92	Q99j92 mus musculu	340	7	2.1	1142	13	Q7SZV2	Q7szv2 xenopus lae
268	7	2.1	539	11	Q99L12	Q99l12 mus musculu	341	7	2.1	1244	11	Q8CHI5	Q8chi5 rattus norv
269	7	2.1	540	16	Q888X4	Q888x4 pseudomonas	342	7	2.1	1271	11	Q8CHR1	Q8chr1 mus musculu
270	7	2.1	541	11	Q9WU61	Q9wu61 rattus norv	343	7	2.1	1277	5	O17517	O17517 caenorhabdi
271	7	2.1	551	4	Q96S66	Q96s66 homo sapien	344	7	2.1	1285	11	Q8K3T3	Q8k3t3 spalax juda
272	7	2.1	572	16	Q8UHB4	Q8uhb4 agrobacteri	345	7	2.1	1345	1	Q54437	Q54437 staphylothe
273	7	2.1	577	16	Q8KE38	Q8ke38 chlorobium	346	7	2.1	1383	12	Q89232	Q89232 canine herp
274	7	2.1	577	16	Q8KAB6	Q8kab6 chlorobium	347	7	2.1	1415	16	O8A9R6	O8a9r6 bacteroides
275	7	2.1	579	5	Q8T7M1	Q8t7m1 physarum po	348	7	2.1	1422	6	Q95KU4	Q95ku4 canis famil
276	7	2.1	582	16	Q8PRA6	Q8pra6 xanthomonas	349	7	2.1	1487	11	Q03626	Q03626 rattus norv
277	7	2.1	588	5	O01465	O01465 caenorhabdi	350	7	2.1	1543	4	Q8WVZ4	Q8wvz4 homo sapien
278	7	2.1	591	11	Q8K3H8	Q8k3h8 cricetus	351	7	2.1	1543	4	Q7Z219	Q7z219 homo sapien
279	7	2.1	600	16	Q8FPD5	Q8fpd5 corynebacte	352	7	2.1	1552	10	O49370	O49370 arabidopsis
280	7	2.1	602	4	Q86VJ9	Q86vj9 homo sapien	353	7	2.1	1560	11	O88323	O88323 mus musculu
281	7	2.1	613	16	Q88C87	Q88c87 rhizobium l	354	7	2.1	1560	11	Q925J9	Q925j9 mus musculu
282	7	2.1	617	11	Q8VDQ7	Q8vdq7 mus musculu	355	7	2.1	1560	11	Q925K0	Q925k0 mus musculu
283	7	2.1	619	5	Q9VJK5	Q9vjk5 drosophila	356	7	2.1	1585	16	Q8UBT4	Q8ubt4 agrobacteri
284	7	2.1	624	5	Q9BNQ2	Q9bnq2 abacion mag	357	7	2.1	1620	5	Q24984	Q24984 giardia lam
285	7	2.1	643	16	Q7UVL7	Q7uvl7 rhodospirill	358	7	2.1	1781	5	O86KF8	O86kf8 dictyosteli
286	7	2.1	643	17	Q9YCH6	Q9ych6 aeropyrum p	359	7	2.1	1785	5	Q7Y85	Q7yy85 cryptospori
287	7	2.1	646	16	Q8KMZ5	Q8kmz5 vibrio chol	360	7	2.1	2055	10	Q7X9V2	Q7x9v2 arabidopsis
288	7	2.1	650	4	Q8NA84	Q8na84 homo sapien	361	7	2.1	2061	10	Q9LTV5	Q9ltv5 arabidopsis
289	7	2.1	656	5	Q9Y114	Q9y114 drosophila	362	7	2.1	2087	5	Q8MXL2	Q8mxl2 leishmania
290	7	2.1	660	16	Q8ZMN7	Q8zmn7 salmonella	363	7	2.1	2747	2	Q9L800	Q9l800 aeromonas s
291	7	2.1	693	4	Q96NV6	Q96nv6 homo sapien	364	7	2.1	3410	5	O18290	O18290 caenorhabdi
292	7	2.1	694	16	Q7UNZ3	Q7unz3 rhodospirill	365	7	2.1	3436	5	O86NG1	O86ng1 caenorhabdi
293	7	2.1	695	8	Q32508	Q32508 lycium cest	366	7	2.1	3436	5	O86NF9	O86nf9 caenorhabdi
294	7	2.1	695	8	Q32700	Q32700 nolana spat	367	7	2.1	3522	5	O86NF7	O86nf7 caenorhabdi
295	7	2.1	695	8	Q33168	Q33168 salpiglossi	368	7	2.1	4091	5	O96204	O96204 plasmodium
296	7	2.1	696	5	O17479	O17479 hyalophora	369	7	2.1	4340	2	O30764	O30764 streptomyc
297	7	2.1	705	5	Q9VLC6	Q9vlc6 drosophila	370	7	2.1	4545	11	O61291	O61291 mus musculu
298	7	2.1	708	17	Q8ZXU4	Q8zxu4 pyrobaculum	371	7	2.1	4918	5	Q867N2	Q867n2 caenorhabdi
299	7	2.1	715	5	Q8WS55	Q8ws55 oikopleura	372	7	2.1	4929	5	Q867D9	Q867d9 caenorhabdi
300	7	2.1	716	16	Q87CY5	Q87cy5 xyrella fas	373	7	2.1	4944	5	Q867D9	Q867d9 caenorhabdi
301	7	2.1	726	2	Q8GFR4	Q8gfr4 citrobacter	374	7	2.1	6145	16	Q93H84	Q93h84 streptomyc
302	7	2.1	728	5	Q8IEM1	Q8iem1 plasmodium	375	7	2.1	6239	16	Q9S0R7	Q9s0r7 streptomyc
303	7	2.1	730	8	O98698	O98698 exacum affi	376	7	2.1	21	4	Q9UMU6	Q9umu6 homo sapien
304	7	2.1	732	4	O9P0Y2	O9p0y2 homo sapien	377	6	1.8	22	8	Q9T2R5	Q9t2r5 solanum tub
305	7	2.1	732	4	Q9BQ33	Q9bq33 homo sapien	378	6	1.8	26	11	Q9QVZ8	Q9qvz8 mus sp. b c
306	7	2.1	737	13	Q802D0	Q802d0 brachydanio	379	6	1.8	29	11	Q88224	Q88224 mus musculu
307	7	2.1	744	4	Q8N261	Q8n261 homo sapien	380	6	1.8	30	8	Q34897	Q34897 lasiorhinus
308	7	2.1	765	5	Q20479	Q20479 caenorhabdi	381	6	1.8				

382	6	1.8	35	8	Q8M1N3	Q8m1n3 limbedesuss	455	86	2	Q9EXM8	Q9exm8 enterobacte
383	6	1.8	36	16	O25409	O25409 helicobacte	456	86	10	Q84JY6	Q84jy6 arabidopsis
384	6	1.8	37	16	Q8F9D8	Q8f9d8 leptospira	457	86	16	Q8RU64	Q8ru64 anabaena sp
385	6	1.8	38	4	Q7Z6X7	Q7z6x7 homo sapien	458	88	2	Q31217	Q31217 desulfovibr
386	6	1.8	39	16	Q98RB8	Q98rb8 mycoplasma	459	88	2	O66207	O66207 klebsiella
387	6	1.8	41	2	Q93LW0	Q93lw0 helicobacte	460	88	2	O66193	O66193 enterobacte
388	6	1.8	41	2	Q93LW5	Q93lw5 helicobacte	461	88	2	O66217	O66217 pantoea ana
389	6	1.8	41	2	Q93LW3	Q93lw3 helicobacte	462	88	2	O66195	O66195 enterobacte
390	6	1.8	43	2	O82949	O82949 chromatium	463	88	2	O66203	O66203 serratia fi
391	6	1.8	44	2	Q93UZ3	Q93uz3 chromatium	464	88	2	O66199	O66199 pantoea agg
392	6	1.8	46	2	Q93LT1	Q93lt1 helicobacte	465	88	2	O66215	O66215 pantoea agg
393	6	1.8	46	2	Q93LS1	Q93ls1 helicobacte	466	88	2	O66219	O66219 erwinia car
394	6	1.8	46	2	Q93LS3	Q93ls3 helicobacte	467	88	2	O66191	O66191 enterobacte
395	6	1.8	46	2	Q93LU0	Q93lu0 helicobacte	468	88	2	O66221	O66221 erwinia aph
396	6	1.8	46	2	Q93LU3	Q93lu3 helicobacte	469	88	2	O66197	O66197 enterobacte
397	6	1.8	46	2	Q93LT2	Q93lt2 helicobacte	470	88	2	O66213	O66213 klebsiella
398	6	1.8	46	2	Q93LT0	Q93lt0 helicobacte	471	88	2	O66201	O66201 serratia ru
399	6	1.8	46	2	Q93LS6	Q93ls6 helicobacte	472	88	2	O66211	O66211 klebsiella
400	6	1.8	48	16	Q8G2J3	Q8g2j3 bruceella su	473	88	2	O66205	O66205 serratia ma
401	6	1.8	49	16	Q8G004	Q8g004 bruceella su	474	88	2	O66209	O66209 klebsiella
402	6	1.8	51	4	Q9UDD2	Q9udd2 homo sapien	475	88	2	O66189	O66189 enterobacte
403	6	1.8	52	12	Q91G27	Q91g27 chilo iride	476	88	2	O33687	O33687 primary end
404	6	1.8	53	12	O8VA91	O8va91 polycymaviru	477	89	5	Q81EE1	Q81ee1 plasmodium
405	6	1.8	53	16	Q82EW7	Q82em7 streptomyc	478	89	10	Q8LJ37	Q8lj37 oryza sativ
406	6	1.8	54	16	Q82AA3	Q82aa3 streptomyc	479	89	16	Q8DJC2	Q8dj2c synecococc
407	6	1.8	56	17	O27388	O27388 methanobact	480	91	5	Q86BD7	Q86bd7 drosophila
408	6	1.8	57	16	Q92X78	Q92x78 rhizobium m	481	91	6	Q9N038	Q9n038 macaca fasc
409	6	1.8	58	2	Q51751	Q51751 pseudomonas	482	91	6	Q9X7B6	Q9x7b6 mycobacteri
410	6	1.8	60	12	Q69131	Q69131 human herpe	483	93	2	Q9Z2M7	Q9z2m7 rattus sp.
411	6	1.8	60	12	O43611	O43611 epstein-bar	484	94	8	O9AJB6	O9ajb6 pseudalter
412	6	1.8	60	12	O8AZ22	O8az22 human herpe	485	95	16	O8FYN4	O8fyn4 bruceella su
413	6	1.8	61	12	O37321	O37321 heliothis a	486	96	2	O8KIW6	O8kiw6 buchnera sp
414	6	1.8	61	16	Q836K7	Q836k7 enterococcu	487	96	2	O8KIW8	O8kiw8 buchnera sp
415	6	1.8	63	5	O96374	O96374 manduca sex	488	96	9	O8W6C5	O8w6c5 bacterioph
416	6	1.8	63	10	Q940T4	Q940t4 arabidopsis	489	96	16	Q83DL6	Q83dl6 coxiella bu
417	6	1.8	64	16	Q8G2O6	Q8g2g6 bruceella su	490	97	2	Q9F4B9	Q9f4b9 bacillus ma
418	6	1.8	66	16	Q9U222	Q9u222 staphylococ	491	97	5	Q8MXM8	Q8mxm8 dictyosteli
419	6	1.8	66	16	Q8WN22	Q8wn22 staphylococ	492	97	16	Q7U349	Q7u349 candidatus
420	6	1.8	67	16	Q8K6N7	Q8k6n7 streptococc	493	98	6	Q8WN12	Q8wn12 ovis aries
421	6	1.8	67	8	Q7Y8G4	Q7y8g4 hemiechinus	494	98	8	O8LWP4	O8lwp4 tupaia bela
422	6	1.8	67	12	Q86132	Q86132 vesicular s	495	98	8	Q9G3R5	Q9g3r5 chalinolobu
423	6	1.8	68	2	Q93LL6	Q93ll6 nostoc punc	496	98	8	O9B991	O9b991 muntiacus v
424	6	1.8	68	13	Q98SP3	Q98sp3 brachydanio	497	98	8	O9B996	O9b996 muntiacus v
425	6	1.8	68	16	Q8DX22	Q8dx22 streptococc	498	98	8	O94YC5	O94yc5 pipistrellu
426	6	1.8	72	5	Q81LAI	Q81lal dictyosteli	499	98	8	O9B991	O9b991 muntiacus m
427	6	1.8	72	10	Q7XUP3	Q7xup3 oryza sativ	500	98	8	O9G422	O9g422 tupaia bela
428	6	1.8	72	10	Q7XSB4	Q7xsb4 oryza sativ	501	98	8	O9BIC5	O9bic5 muntiacus c
429	6	1.8	72	16	Q9HYJ4	Q9hyj4 pseudomonas	502	98	8	O85RW9	O85rw9 muntiacus m
430	6	1.8	72	16	O817F6	O817f6 bacillus ce	503	98	8	O7Y8H3	O7y8h3 elephantulu
431	6	1.8	73	2	Q32310	Q32310 bacillus th	504	98	8	Q7X8I1	Q7x8i1 oryza sativ
432	6	1.8	73	5	Q9XVG6	Q9xvg6 caenorhabdi	505	98	10	Q7X8I1	Q7x8i1 oryza sativ
433	6	1.8	73	8	Q85WY1	Q85wyl pinus korai	506	98	12	Q9QEW0	Q9qew0 porcine res
434	6	1.8	73	9	O03922	O03922 bacterioph	507	98	12	Q9QEW1	Q9qew1 porcine res
435	6	1.8	74	16	Q97P87	Q97p87 streptococc	508	98	12	Q9QEW2	Q9qew2 porcine res
436	6	1.8	75	6	Q9TTQ1	Q9ttq1 equus cabal	509	99	2	O8GFN4	O8gfn4 anabaena cf
437	6	1.8	75	10	O941C7	O941c7 arabidopsis	510	99	2	O8GFI7	O8gfi7 anabaena sp
438	6	1.8	75	16	Q92UZ5	Q92uz5 rhizobium m	511	99	2	O8GFI6	O8gfi6 anabaena sp
439	6	1.8	76	5	O42505	O42505 drosophila	512	99	2	O8GFI5	O8gfi5 anabaena sp
440	6	1.8	77	16	Q8YPP7	Q8ypp7 anabaena sp	513	99	2	O8GFI4	O8gfi4 anabaena sp
441	6	1.8	77	16	Q7Y2F7	Q7y2f7 bacterioph	514	99	2	O8GBZ0	O8gbz0 nostoc sp.
442	6	1.8	78	17	Q8Q0K6	Q8q0k6 methanosarc	515	99	2	O8GBW5	O8gbw5 planktothri
443	6	1.8	81	6	Q9TTQ2	Q9ttq2 equus cabal	516	99	2	O8GBW4	O8gbw4 planktothri
444	6	1.8	82	13	O7ZTT8	O7ztt8 brachydanio	517	99	2	O8GBW3	O8gbw3 planktothri
445	6	1.8	82	16	Q9PPD2	Q9ppd2 campylobact	518	99	2	O8GBW2	O8gbw2 planktothri
446	6	1.8	83	11	O7O182	O7o182 mus musculu	519	99	2	O8GBW1	O8gbw1 planktothri
447	6	1.8	83	17	Q978H2	Q978h2 thermoplasm	520	99	2	O8GBW0	O8gbw0 planktothri
448	6	1.8	84	10	Q94CU0	Q94cu0 oryza sativ	521	99	2	O8GBV9	O8gbv9 planktothri
449	6	1.8	84	12	O8Q540	Q8q540 chimpanzee	522	99	2	O8GBV8	O8gbv8 planktothri
450	6	1.8	85	6	Q9TUZ8	Q9tuz8 ovis aries	523	99	3	O8GBV7	O8gbv7 planktothri
451	6	1.8	85	10	O7XQ19	O7xq19 oryza sativ	524	99	3	O8GBV6	O8gbv6 planktothri
452	6	1.8	86	2	Q9EXM6	Q9exm6 enterobacte	525	99	6	O8KMC8	O8kmc8 equus cabal
453	6	1.8	86	2	Q53845	Q53845 spiroplasma	526	99	6	O8HYQ0	O8hyq0 macaca neme
454	6	1.8	86	2	Q9EUC4	Q9euc4 serratia ma	527	99	8	P92624	P92624 diadora asp

528	6	1.8	99	13	Q8UV71	Q8UV71 brachydanio	601	1.8	116	16	Q8XJV0	Q8xjv0 clostridium
529	6	1.8	99	15	Q8UL16	Q8ul16 human immun	602	1.8	116	16	Q8Z3C0	Q8z3c0 chlamydom
530	6	1.8	99	15	Q8IXS2	Q8ixs2 human immun	603	1.8	117	4	Q96A31	Q96a31 homo sapien
531	6	1.8	99	15	Q8X559	Q8x559 human immun	604	1.8	117	11	Q63063	Q63063 rattus norv
532	6	1.8	100	2	Q831A4	Q831a4 staphylococ	605	1.8	117	16	Q8Y1U1	Q8y1u1 ralsstonia s
533	6	1.8	100	4	Q8P0F3	Q8p0f3 homo sapien	606	1.8	118	6	Q86Z26	Q86z26 pan troglod
534	6	1.8	100	5	Q8IRP7	Q8irp7 drosophila	607	1.8	118	11	Q8R2H0	Q8r2h0 rattus norv
535	6	1.8	100	6	Q85MD5	Q85md5 bos taurus	608	1.8	118	11	Q9CRB3	Q9crb3 mus musculu
536	6	1.8	100	6	Q8YTTQ4	Q8yttq4 equus cabal	609	1.8	118	16	Q8UD05	Q8ud05 agrobacteri
537	6	1.8	100	10	Q8LNS1	Q8lns1 oryza sativ	610	1.8	118	16	Q8UCV9	Q8ucv9 agrobacteri
538	6	1.8	100	16	Q8ZDL6	Q8zdl6 yersinia pe	611	1.8	119	16	Q8PQM8	Q8pqm8 xanthomonas
539	6	1.8	100	16	Q8XPA3	Q8xpa3 salmonella	612	1.8	119	16	Q8PDQ7	Q8pdq7 xanthomonas
540	6	1.8	101	5	Q8MXN8	Q8mxn8 drosophila	613	1.8	119	16	Q7W7B7	Q7w7b7 bordetella
541	6	1.8	101	6	Q85K94	Q85k94 macaca fasc	614	1.8	120	5	Q86JUS	Q86j5 dictyosteli
542	6	1.8	102	13	Q8DFZ5	Q8dfz5 xenopus lae	615	1.8	120	11	Q8C699	Q8c699 mus musculu
543	6	1.8	102	15	Q8YVG5	Q8yvg5 human immun	616	1.8	121	5	Q95T00	Q95td0 drosophila
544	6	1.8	102	15	Q81931	Q81931 human immun	617	1.8	121	5	Q9AF23	Q9af23 uncultured
545	6	1.8	103	5	Q81PR1	Q81pr1 drosophila	618	1.8	122	2	Q8WU89	Q8wu89 homo sapien
546	6	1.8	103	15	Q81930	Q81930 human immun	619	1.8	122	4	Q8NV16	Q8nv16 homo sapien
547	6	1.8	103	16	Q8XK86	Q8xk86 clostridium	620	1.8	122	4	Q8N8P7	Q8n8p7 homo sapien
548	6	1.8	103	16	Q89MS9	Q89ms9 bradyrhizob	621	1.8	122	11	Q8CID7	Q8cid7 mus musculu
549	6	1.8	104	5	Q8T4J5	Q8t4j5 scylla serr	622	1.8	122	16	Q9HZU9	Q9hzu9 pseudomonas
550	6	1.8	104	10	Q42028	Q42028 arabidopsis	623	1.8	122	16	Q89VH2	Q89vh2 bacteroides
551	6	1.8	104	15	Q81934	Q81934 human immun	624	1.8	122	17	Q8U1X6	Q8u1x6 pyrococcus
552	6	1.8	104	15	Q81934	Q81934 human immun	625	1.8	122	17	Q8PS76	Q8ps76 methanarsarc
553	6	1.8	104	16	Q8F8M5	Q8f8m5 streptomyce	626	1.8	123	11	Q90137	Q90137 marmota mon
554	6	1.8	105	4	Q60384	Q60384 homo sapien	627	1.8	123	13	Q9DDX9	Q9ddx9 xenopus lae
555	6	1.8	106	2	Q847N9	Q847n9 aster vello	628	1.8	123	16	Q9RT46	Q9rt46 deinococcus
556	6	1.8	106	15	Q81932	Q81932 human immun	629	1.8	123	16	Q65085	Q65085 foot-and-mo
557	6	1.8	106	15	Q81932	Q81932 human immun	630	1.8	124	12	Q65085	Q65085 foot-and-mo
558	6	1.8	106	16	Q81932	Q81932 human immun	631	1.8	124	16	Q92B29	Q92b29 listeria in
559	6	1.8	107	11	Q82125	Q82125 rickettsia	632	1.8	124	16	Q7WFD6	Q7wfd6 bordetella
560	6	1.8	107	12	Q81934	Q81934 human immun	633	1.8	125	5	Q9U1P6	Q9u1p6 caenorhabdi
561	6	1.8	107	15	Q8YVG7	Q8yvg7 human immun	634	1.8	125	13	Q9DFZ6	Q9dfz6 xenopus lae
562	6	1.8	107	15	Q81910	Q81910 human immun	635	1.8	126	1	P95861	P95861 sulfolobus
563	6	1.8	107	15	Q8Y1L5	Q8y1l5 human immun	636	1.8	126	10	Q7Y1C7	Q7y1c7 oryza sativ
564	6	1.8	107	15	Q8YVF6	Q8yvf6 human immun	637	1.8	126	16	Q7UB47	Q7ub47 shigella fl
565	6	1.8	107	15	Q8Y1927	Q8y1927 human immun	638	1.8	127	12	Q9YEE3	Q9yee3 aeropyrum p
566	6	1.8	107	15	Q8YVH2	Q8yvfh2 human immun	639	1.8	127	12	O10461	O10461 venezuelan
567	6	1.8	107	15	Q81920	Q81920 human immun	640	1.8	127	12	O10457	O10457 venezuelan
568	6	1.8	107	16	Q81651	Q81651 borrelia bu	641	1.8	127	12	O10460	O10460 venezuelan
569	6	1.8	107	16	Q88J53	Q88j53 pseudomonas	642	1.8	127	13	Q9DDY1	Q9ddy1 encephalomy
570	6	1.8	108	2	Q8KVR7	Q8kvr7 bacteroides	643	1.8	127	16	Q8E1W3	Q8e1w3 shewanella
571	6	1.8	108	2	Q45800	Q45800 bacteroides	644	1.8	128	2	Q7X3J9	Q7x3j9 pseudomonas
572	6	1.8	108	2	Q44706	Q44706 borrelia bu	645	1.8	128	9	Q9B030	Q9b030 bacterioph
573	6	1.8	108	11	Q8CV78	Q8cv78 mus musculu	646	1.8	128	10	Q94163	Q94163 oryza sativ
574	6	1.8	109	4	Q727Q8	Q727q8 homo sapien	647	1.8	128	11	Q8C2V3	Q8c2v3 mus musculu
575	6	1.8	109	16	Q88CE9	Q88ce9 pseudomonas	648	1.8	128	16	Q9RVX6	Q9rvx6 deinococcus
576	6	1.8	109	17	Q58093	Q58093 pyrococcus	649	1.8	128	16	Q928A1	Q928a1 listeria in
577	6	1.8	110	5	Q8T416	Q8t416 drosophila	650	1.8	128	16	Q8Y4F2	Q8y4f2 listeria mo
578	6	1.8	110	13	Q42454	Q42454 trachemys s	651	1.8	129	2	Q84GY0	Q84gy0 photorhabdu
579	6	1.8	111	10	Q8LHY8	Q8lhy8 oryza sativ	652	1.8	129	5	Q86K85	Q86k85 dictyosteli
580	6	1.8	111	11	Q811A7	Q811a7 rattus norv	653	1.8	129	6	Q862M3	Q862m3 bos taurus
581	6	1.8	111	16	Q8HWS5	Q8hws5 pseudomonas	654	1.8	129	16	Q8NNM5	Q8nnm5 corynebacte
582	6	1.8	111	17	Q9UY95	Q9uy95 pyrococcus	655	1.8	129	17	Q8TR81	Q8tr81 methanarsarc
583	6	1.8	112	2	Q931B3	Q931b3 staphylococ	656	1.8	132	5	Q8T9B2	Q8t9b2 drosophila
584	6	1.8	112	3	Q83884	Q83884 saccharomyc	657	1.8	132	5	Q9W2M8	Q9w2m8 drosophila
585	6	1.8	112	16	Q8Y018	Q8y018 ralsstonia s	658	1.8	132	8	Q7Y7V2	Q7y7v2 cunningham
586	6	1.8	112	17	Q8ZTR9	Q8ztr9 pyrobaculum	659	1.8	132	12	Q39815	Q39815 encephalomy
587	6	1.8	113	2	Q8KQR1	Q8kqr1 lactobacilli	660	1.8	132	16	Q9RT34	Q9rt34 deinococcus
588	6	1.8	113	8	Q35015	Q35015 meloidogyne	661	1.8	132	16	Q9KA40	Q9ka40 bacillus ha
589	6	1.8	113	16	Q8ZPH6	Q8zph6 salmonella	662	1.8	132	16	Q9A895	Q9a895 caulobacter
590	6	1.8	113	16	Q88626	Q88626 pseudomonas	663	1.8	133	2	Q55212	Q55212 streptococ
591	6	1.8	113	16	Q7WKS8	Q7wks8 bordetella	664	1.8	133	16	Q7UVZ6	Q7uvz6 rhodopirell
592	6	1.8	113	16	Q7W8U8	Q7w8u8 bordetella	665	1.8	134	10	Q9ARU5	Q9aru5 oryza sativ
593	6	1.8	113	16	Q7VXG6	Q7vxg6 bordetella	666	1.8	134	13	Q9DDX4	Q9ddx4 xenopus lae
594	6	1.8	114	4	Q81WS4	Q81ws4 homo sapien	667	1.8	134	16	Q69567	Q69567 mycobacteri
595	6	1.8	114	10	Q94AF8	Q94af8 arabidopsis	668	1.8	134	16	Q7V2U6	Q7v2u6 prochloroco
596	6	1.8	114	16	Q7USA6	Q7usa6 rhodopirell	669	1.8	135	6	Q29049	Q29049 sus scrofa
597	6	1.8	115	15	Q7ZEJ9	Q7zej9 human immun	670	1.8	135	16	P95012	P95012 mycobacteri
598	6	1.8	115	16	Q8YJ66	Q8yj66 brucella me	671	1.8	135	16	Q91380	Q91380 pseudomonas
599	6	1.8	115	16	Q8CMN1	Q8cmn1 staphylococ	672	1.8	135	16	Q9CBH3	Q9cbh3 mycobacteri
600	6	1.8	116	5	Q7YX03	Q7yx03 caenorhabdi	673	1.8	135	16	Q8DVR5	Q8dvr5 streptococ

674 Q7tyc5 mycobacteri
675 O45582 caenorhabdi
676 Q9xyh8 leishmania
677 Q8wna0 cynocephalu
678 Q9cqx5 mus musculus
679 Q9ddx3 xenopus lae
680 Q9bi29 chlamys isl
681 Q9e2h0 hepatitis c
682 Q8cvy5 escherichia
683 Q88md0 pseudomonas
684 Q83km3 shigella fl
685 Q93ki8 uncultured
686 Q9lcs6 west nile v
687 Q7r7n4 bubaline he
688 Q9ddy2 xenopus lae
689 Q8zza5 pyrobaculum
690 Q99q68 uncultured
691 Q9af44 uncultured
692 Q9af45 uncultured
693 Q9af46 uncultured
694 Q9bng1 carcinoscor
695 Q9bnf2 cithonius t
696 Q89s26 bradyrhizob
697 Q88f26 pseudomonas
698 Q92276 saccharomyc
699 Q9k0f8 neisseria m
700 Q8u957 agrobacteri

DR EMBL: AF390894; AAL26989.1; -
DR GO: GO:0004872; P.receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Receptor.
SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF74BE8D4 CRC64;
Query Match 100.0%; Score 335; DB 4; Length 335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAGSPCTLTLYILWLTGSAAGPVKELVSGVGGVATPPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTLTLYILWLTGSAAGPVKELVSGVGGVATPPLKSKVKQVDSIVWTFNTTPL 60
Qy 61 VTIQPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQY 120
Db 61 VTIQPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQY 120
Qy 121 VLHYEHLSPKVTMGLOSNKNGTCVNTLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Db 121 VLHYEHLSPKVTMGLOSNKNGTCVNTLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Qy 181 PISRWGESDWTFCVARNPVSFNPSPIARLCEGAADDPDSSMVLCLLVPLLSL 240
Db 181 PISRWGESDWTFCVARNPVSFNPSPIARLCEGAADDPDSSMVLCLLVPLLSL 240
Qy 241 FVLGLFLWFLKREQEYIEBKRVVDICRTPNICPHSGENTYDTPHNTIRILKEDPA 300
Db 241 FVLGLFLWFLKREQEYIEBKRVVDICRTPNICPHSGENTYDTPHNTIRILKEDPA 300
Qy 301 NTYVSTVEIPKMEPHSLTMDPTPLPAYENVI 335
Db 301 NTYVSTVEIPKMEPHSLTMDPTPLPAYENVI 335

ALIGNMENTS

RESULT 1
Q9NQ25 PRELIMINARY; PRT; 335 AA.
AC Q9NQ25
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BA404F10.4 (Novel LY9 (lymphocyte antigen 9) like protein) (NK cell
DE Receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
DE cytoxic cell).
GN BA404F10.4 OP/CSI.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bates K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Boles K.S.; Mathew P.A. Sr.;
RL "Cloning of a new member of the CD2 subset of receptors expressed on
RT NK cells";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RA Fujii Y., Takayama K., Teuritani K., Yajima Y., Amemiya T., Ukai Y.,
RA Naito K., Kawaguchi A.;
RT "Homo sapiens mRNA for FOAP-12 protein, complete cds.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
RT "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
RT Independent Receptor of the CD2 Family.";
RL J. Immunol. 167:0-0(2001).
DR EMBL; AL121985; CAC00579.1; -
DR EMBL; AF291815; AAK11549.1; -
DR EMBL; AB027233; BAB61022.1; -

RESULT 2
Q8N6Y8 PRELIMINARY; PRT; 296 AA.
AC Q8N6Y8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 19A24 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027867; AAH27867.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 296 AA; 32581 MW; E85D277192494EBC CRC64;

Query Match 76.7%; Score 257; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAGSPCTLTLYILWLTGSAAGPVKELVSGVGGVATPPLKSKVKQVDSIVWTFNTTPL 60
Db 1 MAGSPCTLTLYILWLTGSAAGPVKELVSGVGGVATPPLKSKVKQVDSIVWTFNTTPL 60
Qy 61 VTIQPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQY 120
Db 61 VTIQPEGGTTIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQY 120
Qy 121 VLHYEHLSPKVTMGLOSNKNGTCVNTLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180

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Db 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
Db 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKPKRQEE 257
Db 241 FVLGLFLWFLKPKRQEE 257

RESULT 3
QY08
ID QY08
AC QY08
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 19A24 protein.
GN 19A24.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271869; CAB76561.1; -.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 76.7%; Score 257; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
Db 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
QY 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
Db 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
QY 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Db 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
Db 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKPKRQEE 257
Db 241 FVLGLFLWFLKPKRQEE 257

RESULT 4
QY08
ID QY08
AC QY08
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 19A protein.
GN 19A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271869; CAB76561.1; -.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 76.7%; Score 257; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.5e-259;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
Db 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
QY 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
Db 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
QY 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Db 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
Db 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKPKRQEE 257
Db 241 FVLGLFLWFLKPKRQEE 257

RESULT 5
QY08
ID QY08
AC QY08
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP667F126.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloesker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 62.7%; Score 210; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4e-210;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RT member with structural similarity to CD2."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271869; CAB76561.1; -.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37403 MW; BB758E505CA4DDD5 CRC64;

Query Match 69.9%; Score 234; DB 4; Length 335;
Best Local Similarity 99.7%; Pred. No. 5.4e-235;
Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
Db 1 MAGSPTCLTLIYLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIVTNTTTP 60
QY 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
Db 61 VTIOPEGGTIIVTQNRNRERVDPPDGGYSLKSLKQNDSDGIYVYSSSLQQPSTORY 120
QY 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Db 121 VLHVEHLSPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
QY 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
Db 181 PISRWGESDMTFCICARNPVRNPFSSPILARKLCEGAADDPDSSNVLLCLLLVPLLSSL 240
QY 241 FVLGLFLWFLKPKRQEE 257
Db 241 FVLGLFLWFLKPKRQEE 257

RESULT 5
QY08
ID QY08
AC QY08
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP667F126.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloesker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7BBFC14 CRC64;

Query Match 62.7%; Score 210; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 4e-210;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 126 EHLSPKVTMGLOSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSILPISWR 185
 DB 19 EHLSPKVTMGLOSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOANESHNGSILPISWR 78
 QY 186 WGESDMTFCVARNPVSNFSSPILARKLCEGAADDDPSSSVLCLLVPLLLSLFVLGL 245
 DB 79 WGESDMTFCVARNPVSNFSSPILARKLCEGAADDDPSSSVLCLLVPLLLSLFVLGL 138
 QY 246 FLWFLKRRQBYIEEKKRVDCIRTPNICPHSGENTYDITPHTNRTILKEDPANTVYS 305
 DB 139 FLWFLKRRQBYIEEKKRVDCIRTPNICPHSGENTYDITPHTNRTILKEDPANTVYS 198
 QY 306 TVEIPKQENPHSLTMDPTPLFAYENVI 335
 DB 199 TVEIPKQENPHSLTMDPTPLFAYENVI 228

RESULT 6
 Q9YC18 PRELIMINARY; PRT; 156 AA.
 AC Q9YC18;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein APE1433.
 GN APE1433.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 Jin-no K., Takanashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000061; BAA80430.1; -;
 DR PIR; H72621; H72621.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 156 AA; 15954 MW; 73BBB5C99FBE453D CRC64;

Query Match 2.7%; Score 9; DB 17; Length 156;
 Best Local Similarity 100.0%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 LTGSAASGP 25
 DB 105 LTGSAASGP 113

RESULT 7
 Q91XA0 PRELIMINARY; PRT; 294 AA.
 AC Q91XA0;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to 19A24 protein.
 GN 4930560D03RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Salivary gland;
 RA Strausberg R.; 2001 to the EMBL/GenBank/DBSJ databases.
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC011154; AAH11154.1; -;
 DR MGI; MGI:1922595; 4930560D03RIK.
 DR InterPro; IPR007110; IG-like.
 DR PROSITE; PS50835; IG LIKE; 1.
 SQ SEQUENCE 294 AA; 32782 MW; F4C88BC4CFAA1AFB CRC64;
 Query Match 2.7%; Score 9; DB 11; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
 DB 135 QSNKNGTCV 143
 RESULT 8
 Q8CJ63 PRELIMINARY; PRT; 300 AA.
 AC Q8CJ63;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Leukocyte cell-surface antigen isoform 8.
 GN 4930560D03RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA16/c; TISSUE=Thymus;
 RX MEDLINE=22226696; PubMed=12242590;
 RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
 Bosch J., Terhorst C., Engel P.;
 RT "Mouse novel Ly-9, a new member of the expanding CD150 (SLAM) family of
 leukocyte cell-surface receptors.";
 RL Immunogenetics 54:394-402(2002).
 DR EMBL; AF467911; AAM63160.1; -;
 DR PIR; PT0566; PT0566.
 DR MGI; MGI:1922595; 4930560D03RIK.
 DR InterPro; IPR007110; IG-like.
 DR PROSITE; PS50835; IG LIKE; 1.
 SQ SEQUENCE 300 AA; 33332 MW; 9948108710BEBBC3D CRC64;

Query Match 2.7%; Score 9; DB 11; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
 DB 135 QSNKNGTCV 143

RESULT 9
 Q8BHK6 PRELIMINARY; PRT; 333 AA.
 AC Q8BHK6;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Similar to 19A24 protein homolog.
 GN 4930560D03RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Aorta;
 RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium.
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030135; BAC26801.1; --
DR EMBL; AK030148; BAC26810.1; --
DR EMBL; AK040678; BAC30665.1; --
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 333 AA; 37217 MW; 0C9A0A0AFACD46E CRC64;

Query Match 2.7%; Score 9; DB 11; Length 333;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
Db 135 QSNKNGTCV 143

RESULT 10
Q8CJ65
ID Q8CJ65 PRELIMINARY; PRT; 335 AA.
AC Q8CJ65;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
GN 4930560D03Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
Bosch J., Terhorst C., Engel P.;
RT "Mouse novel ly9: a new member of the expanding CD150 (SLAM) family of
leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467909; AAN63158.1; --
DR PIR; PT0566; PT0566
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37493 MW; C210E9CEADC8F3EB CRC64;

Query Match 2.7%; Score 9; DB 11; Length 335;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
Db 135 QSNKNGTCV 143

RESULT 11
Q8CJ64
ID Q8CJ64 PRELIMINARY; PRT; 335 AA.
AC Q8CJ64;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
GN 4930560D03Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
Bosch J., Terhorst C., Engel P.;
RT "Mouse novel ly9: a new member of the expanding CD150 (SLAM) family of
leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467910; AAN63159.1; --
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37590 MW; 85F00ABDFC8B90A0 CRC64;

Query Match 2.7%; Score 9; DB 11; Length 335;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
Db 135 QSNKNGTCV 143

RESULT 12
Q8BT12
ID Q8BT12 PRELIMINARY; PRT; 335 AA.
AC Q8BT12;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK089525; BAC40914.1; --
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03Rik.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37521 MW; 99E8802E55A98A03 CRC64;

Query Match 2.7%; Score 9; DB 11; Length 335;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 QSNKNGTCV 146
Db 135 QSNKNGTCV 143

RESULT 13
Q884T6
ID Q884T6 PRELIMINARY; PRT; 83 AA.
AC Q884T6;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Prevent-host-death family protein.
GN PSPTO2000.

```

OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidse T.,
RA White O., Fraser C., Collier A.;
RT "Complete sequence of Pseudomonas syringae.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS016862; AAO55518.1; -
DR TIGR; PSPT02000; -
KW Complete proteome.
SQ SEQUENCE 83 AA; 8993 MW; ED9080CB44BCD3EE CRC64;

Query Match 2.4%; Score 8; DB 16; Length 83;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QLTGSAAS 23
Db |||||
46 QLTGSAAS 53

RESULT 14
Q94E37 PRELIMINARY; PRT; 91 AA.
AC Q94E37;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE OSJNEB0032H19.17 protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
RT clone:OSJNEB0032H19.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003219; BAB61185.1; -
DR Gramene; Q94E37; -
SQ SEQUENCE 91 AA; 9789 MW; D9D559FB49BF71B2 CRC64;

Query Match 2.4%; Score 8; DB 10; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 236 LLLSLFVL 243
Db |||||
16 LLLSLFVL 23

RESULT 15
Q8IVUO PRELIMINARY; PRT; 129 AA.
AC Q8IVUO;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Similar to papilin, proteoglycan-like sulfated glycoprotein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042057; AAH42057.1; -
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
SQ SEQUENCE 129 AA; 14368 MW; D51144A494C12B3B CRC64;

Query Match 2.4%; Score 8; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LLLVPLLL 238
Db |||||
4 LLLVPLLL 11

Search completed: August 18, 2004, 16:00:33
Job time : 46 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2004, 15:48:32 ; Search time 39 Seconds
(without alignments)
2710.220 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPTCLTIYIQLTGS.....PHSLTMDPTPLPAYENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1772	100.0	335	4	Q9NQ25
2	1769	99.8	335	4	Q9NY08
3	1392.5	78.6	328	4	Q9NY23
4	1349	76.1	296	4	Q8NGY8
5	1160.5	65.5	228	4	Q8ND32
6	817	46.1	333	11	Q8BHK6
7	778.5	43.9	335	11	Q8CJ64
8	773.5	43.7	335	11	Q8BRL2
9	769.5	43.4	335	11	Q8CJ65
10	651	36.7	300	11	Q8CJ63
11	637.5	36.0	294	11	Q91XA0
12	362.5	20.5	328	4	O15430
13	362.5	20.5	328	7	Q8WLP1
14	362.5	20.5	329	11	Q9Z178
15	359	20.3	339	4	Q8WW18
16	358	20.2	345	4	Q9UIB8

17	354.5	20.0	649	11	Q7TMP7	Q7tmp7 mus musculus
18	353.5	19.9	544	11	Q8C2D4	Q8c2d4 mus musculus
19	330.5	18.7	289	4	Q96A28	Q96a28 homo sapien
20	329	18.6	538	11	Q8C9E4	Q8c9e4 mus musculus
21	315.5	17.8	331	4	Q96DVO	Q96dvo homo sapien
22	311.5	17.6	285	11	Q8BTK0	Q8btk0 mus musculus
23	311	17.6	332	4	Q96DU3	Q96du3 homo sapien
24	308.5	17.4	285	11	Q8VE93	Q8ve93 mus musculus
25	308	17.4	280	4	Q95660	Q95660 homo sapien
26	307.5	17.4	285	11	Q9D780	Q9d780 mus musculus
27	304	17.2	272	4	Q9UIB7	Q9uib7 homo sapien
28	290.5	16.4	241	4	Q9UIB6	Q9uib6 homo sapien
29	281	15.9	197	4	Q9UII7	Q9uit7 homo sapien
30	225.5	12.7	331	11	Q9ET40	Q9et40 mus musculus
31	225.5	12.7	351	11	Q9ET39	Q9et39 mus musculus
32	204.5	11.5	338	6	Q95MM6	Q95mm6 bos taurus
33	187.5	10.6	336	6	Q9GJT3	Q9gjt3 saguinus oe
34	183.5	10.4	335	4	Q86QR3	Q86qr3 homo sapien
35	183	10.3	266	11	Q9CUC8	Q9cuc8 mus musculus
36	179	10.1	278	11	Q9D3G2	Q9d3g2 mus musculus
37	178	10.0	278	11	Q8R3T7	Q8r3t7 mus musculus
38	171	9.7	329	4	Q9NQD2	Q9nqd2 homo sapien
39	170	9.6	365	4	Q9Y288	Q9y288 homo sapien
40	168.5	9.5	342	6	Q95L99	Q95l99 canis famil
41	167.5	9.5	342	6	Q95MM9	Q95mm9 canis famil
42	159.5	9.0	370	4	Q9BZM8	Q9bzm8 homo sapien
43	158.5	8.9	326	11	Q8CAU4	Q8cau4 mus musculus
44	152	8.6	288	4	Q9NQ26	Q9nq26 homo sapien
45	150.5	8.5	285	4	Q9P0V8	Q9p0v8 homo sapien
46	145.5	8.2	416	4	Q8N7I3	Q8n7i3 homo sapien
47	144	8.1	344	11	Q9R201	Q9r201 mus musculus
48	142	8.0	207	4	Q9HBE9	Q9hbe9 homo sapien
49	133.5	7.5	394	11	Q9EQK9	Q9eqk9 rattus norv
50	132.5	7.5	372	13	Q9OY50	Q9oy50 brachydanio
51	128.5	7.3	253	6	Q28753	Q28753 ovis sp. lf
52	126.5	7.1	461	4	Q8O430	Q8o430 homo sapien
53	125.5	7.1	430	4	Q15600	Q15600 homo sapien
54	125.5	7.1	464	4	Q16170	Q16170 homo sapien
55	125.5	7.1	468	4	Q96CA7	Q96ca7 homo sapien
56	124.5	7.0	344	4	Q13774	Q13774 homo sapien
57	124.5	7.0	461	4	Q13854	Q13854 homo sapien
58	123.5	7.0	227	6	Q28754	Q28754 ovis sp. lf
59	123	6.9	140	11	Q8BFV0	Q8bfv0 mus musculus
60	123	6.9	311	11	Q9JLM2	Q9jlm2 rattus norv
61	122.5	6.9	298	13	Q8O4R4	Q8o4r4 brachydanio
62	122.5	6.9	458	11	Q61351	Q61351 mus musculus
63	122.5	6.9	521	11	Q61352	Q61352 mus musculus
64	122	6.9	326	6	Q9N166	Q9n166 papio hamad
65	122	6.9	344	4	Q9UKV4	Q9ukv4 homo sapien
66	121.5	6.9	377	11	Q8OV04	Q8ov04 mus musculus
67	121.5	6.9	536	11	Q8BJE2	Q8bje2 mus musculus
68	119.5	6.7	332	13	Q9IB08	Q9ib08 spherooides
69	118.5	6.7	520	11	Q925P2	Q925p2 mus musculus
70	115	6.5	357	13	Q9OZL5	Q9ozl5 anas platyr
71	114.5	6.5	430	4	Q8N4F1	Q8n4f1 homo sapien
72	114.5	6.5	702	4	Q8N4D0	Q8n4d0 homo sapien
73	113.5	6.4	454	11	Q91W54	Q91w54 mus musculus
74	113.5	6.4	521	11	Q925P3	Q925p3 mus musculus
75	113	6.4	373	4	Q9H6B4	Q9h6b4 homo sapien
76	113	6.4	621	11	Q811I7	Q811i7 mus musculus
77	111	6.3	372	11	Q8K1G0	Q8k1g0 rattus norv
78	110	6.2	539	6	Q8HXQ6	Q8hxq6 sus scrofa
79	109	6.2	316	11	Q8VE98	Q8ve98 mus musculus
80	109	6.2	924	10	Q7XTP5	Q7xtp5 oryza sativ
81	108.5	6.1	365	6	Q8WMV3	Q8wmv3 bos taurus
82	108	6.1	304	11	Q9CVA4	Q9cva4 mus musculus
83	108	6.1	316	11	Q7TPB4	Q7tpb4 rattus norv
84	107.5	6.1	398	11	Q07763	Q07763 mus musculus
85	107	6.0	399	11	Q9ESES	Q9eses mus musculus
86	106.5	6.0	752	5	Q9XYS4	Q9xys4 hydra atten
87	106.5	6.0	4138	5	Q811Y3	Q811y3 plasmodium
88	106	6.0	397	11	Q9JIE0	Q9jie0 mus musculus
89	106	6.0	897	10	Q9SJY2	Q9sfj2 arabidopsis

90	105.5	6.0	335	13	Q9PWR4	Q9pwr4 gallus gall	163	92.5	5.2	782	12	Q8JVB8	Q8jvb8 porcine lym
91	105.5	6.0	340	11	Q9JIE1	Q9jie1 mus musculus	164	92.5	5.2	782	12	Q8B3U9	Q8biu9 porcine lym
92	105	5.9	340	11	Q8B654	Q8b654 mus musculus	165	92	5.2	297	11	Q63476	Q63476 rattus norv
93	104.5	5.9	319	6	Q9TU79	Q9tu79 sus scrofa	166	92	5.2	426	4	Q60410	Q60410 homo sapien
94	104.5	5.9	1271	16	Q8A321	Q8a321 bacteroides	167	92	5.2	607	12	Q9YK07	Q9ykd7 rinderpest
95	104	5.9	455	11	Q920L8	Q920l8 mus musculus	168	92	5.2	667	11	Q8CHA6	Q8cha6 mus musculus
96	104	5.9	535	11	Q9EQT7	Q9eqt7 mus musculus	169	92	5.2	700	11	Q7TSU7	Q7tsu7 mus musculus
97	103.5	5.8	319	6	Q9TU80	Q9tu80 canis famil	170	92	5.2	822	10	Q9ZQX3	Q9zqx3 arabidopsis
98	103.5	5.8	323	6	Q9BDB8	Q9bdb8 cercocobus	171	92	5.2	1020	11	Q8BIE6	Q8bie6 mus musculus
99	103.5	5.8	373	11	Q8R373	Q8r373 mus musculus	172	92	5.2	1087	13	Q7ZY71	Q7zy71 xenopus lae
100	103.5	5.8	406	4	Q8N7T8	Q8n7t8 homo sapien	173	92	5.2	2828	4	Q9NR99	Q9nr99 homo sapien
101	103	5.8	1062	13	Q8AXC7	Q8axc7 fugu rubrip	174	91.5	5.2	226	11	Q8C254	Q8c254 mus musculus
102	103	5.8	1078	13	Q8AXC8	Q8axc8 fugu rubrip	175	91.5	5.2	226	11	Q8NH11	Q8nh11 homo sapien
103	102.5	5.8	304	12	Q8TSP1	Q8tsp1 african swi	176	91.5	5.2	230	13	Q90Z86	Q90z86 brachydanio
104	102.5	5.8	323	6	Q9BDM4	Q9bdm4 macaca mula	177	91.5	5.2	230	13	Q8UW30	Q8uw30 brachydanio
105	102.5	5.8	335	13	Q9TGH1	Q9tgh1 gallus gall	178	91.5	5.2	1079	12	Q9YWS6	Q9yws6 melanoplus
106	102.5	5.8	373	11	Q920S5	Q920s5 mus musculus	179	91	5.1	388	4	Q8NC34	Q8nc34 homo sapien
107	102	5.8	1482	5	Q9V4Y0	Q9v4y0 drosophila	180	91	5.1	467	11	Q91VT9	Q91vt9 mus musculus
108	101.5	5.7	761	10	Q22271	Q22271 arabidopsis	181	91	5.1	467	11	Q8C6P2	Q8c6p2 mus musculus
109	100.5	5.7	259	16	Q9CFA4	Q9cfa4 lactococcus	182	91	5.1	510	6	Q8BGV6	Q8bgv6 macaca fasc
110	100.5	5.7	280	13	Q8UML2	Q8uml2 ictalurus p	183	91	5.1	1496	4	Q92626	Q92626 homo sapien
111	100.5	5.7	323	6	Q9BDM2	Q9bdm2 cercopithec	184	91	5.1	1840	11	Q9JIO3	Q9jio3 rattus norv
112	99.5	5.6	323	6	Q9BDM9	Q9bdm9 macaca neme	185	91	5.1	1842	4	Q8IZY3	Q8izy3 homo sapien
113	99.5	5.6	335	13	Q9YGV5	Q9ygv5 gallus gall	186	91	5.1	2053	4	Q8WXU7	Q8wxu7 homo sapien
114	99.5	5.6	658	5	Q8G755	Q8g755 dictyosteli	187	91	5.1	2053	4	Q8IZY4	Q8izy4 homo sapien
115	98.5	5.6	229	11	Q8BNV8	Q8bnv8 mus musculus	188	91	5.1	2113	4	Q8TD84	Q8td84 homo sapien
116	98.5	5.6	348	4	Q9AST1	Q9ast1 homo sapien	189	90.5	5.1	230	13	Q80LW9	Q80lw9 brachydanio
117	98.5	5.6	404	4	Q9GZZ9	Q9gzz9 homo sapien	190	90.5	5.1	306	11	Q7TSA3	Q7tsa3 mus musculus
118	98.5	5.6	733	6	Q8SQ83	Q8sq83 trichosurus	191	90.5	5.1	412	11	Q63611	Q63611 rattus norv
119	98.5	5.6	1227	5	Q21038	Q21038 caenorhabdi	192	90.5	5.1	412	11	Q9RIE1	Q9rie1 rattus norv
120	98.5	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila	193	90.5	5.1	417	4	Q96BJ1	Q96bj1 homo sapien
121	97.5	5.5	2772	5	Q9VAV4	Q9vav4 drosophila	194	90.5	5.1	483	13	Q7SX76	Q7sx76 brachydanio
122	97.5	5.5	2776	5	Q8G9A0	Q8g9a0 drosophila	195	90.5	5.1	922	10	Q9LTL7	Q9ltl7 arabidopsis
123	97.5	5.5	2998	5	Q868Z9	Q868z9 drosophila	196	90.5	5.1	1016	11	Q8C310	Q8c310 mus musculus
124	97	5.5	352	11	Q9JW66	Q9jw66 mus musculus	197	90	5.1	309	11	Q91YV7	Q91yv7 mus musculus
125	97	5.5	484	5	Q26475	Q26475 schistocerc	198	90	5.1	348	11	Q80Z24	Q80z24 mus musculus
126	96.5	5.4	204	11	Q9JLM3	Q9jlm3 rattus norv	199	90	5.1	428	4	Q9P1W5	Q9p1w5 homo sapien
127	96.5	5.4	402	12	Q89501	Q89501 african swi	200	90	5.1	609	12	Q9WHH7	Q9whh7 rinderpest
128	96.5	5.4	533	4	Q8NCB6	Q8ncb6 homo sapien	201	90	5.1	1431	11	Q80U60	Q8ou60 mus musculus
129	96.5	5.4	534	4	Q8NBI8	Q8nbi8 homo sapien	202	89.5	5.1	756	16	Q8CJW2	Q8cjw2 streptomyce
130	96.5	5.4	1896	13	Q9IAJ1	Q9iaj1 xenopus lae	203	89.5	5.1	770	16	Q89LN9	Q89ln9 bradyrhizob
131	96	5.4	339	13	Q9IAZ7	Q9iaz7 spherooides	204	89.5	5.1	833	5	Q9BPQ7	Q9bpq7 halocynthia
132	96	5.4	341	11	Q61354	Q61354 mus musculus	205	89.5	5.1	845	4	Q9H156	Q9h156 homo sapien
133	96	5.4	359	5	Q9V6C2	Q9v6c2 drosophila	206	89.5	5.1	2214	4	Q95425	Q95425 homo sapien
134	96	5.4	526	4	Q9H458	Q9h458 homo sapien	207	89	5.0	240	4	Q9BRW0	Q9brw0 homo sapien
135	95.5	5.4	248	11	Q9D0T4	Q9d0t4 mus musculus	208	89	5.0	292	11	Q80T70	Q80t70 mus musculus
136	95.5	5.4	340	11	Q61349	Q61349 mus musculus	209	89	5.0	314	11	Q61238	Q61238 mus musculus
137	95.5	5.4	365	11	Q9DBJ8	Q9dbj8 mus musculus	210	89	5.0	315	4	Q96DM5	Q96dm5 homo sapien
138	95.5	5.4	448	11	Q9JHL7	Q9jhl7 rattus norv	211	89	5.0	322	13	Q9PTR8	Q9ptr8 spherooides
139	95.5	5.4	458	11	Q63093	Q63093 rattus norv	212	89	5.0	323	5	Q8MKZ7	Q8mkz7 drosophila
140	95.5	5.4	459	11	Q9JHL6	Q9jhl6 rattus norv	213	89	5.0	325	4	Q95791	Q95791 homo sapien
141	95	5.4	814	4	Q8IVU1	Q8ivu1 homo sapien	214	89	5.0	328	11	Q9Z109	Q9z109 mus musculus
142	94.5	5.3	280	13	Q8UWK3	Q8uwk3 ictalurus p	215	89	5.0	356	11	Q64381	Q64381 mus musculus
143	94.5	5.3	286	6	Q46535	Q46535 bos taurus	216	89	5.0	5175	5	Q810L3	Q810l3 caenorhabdi
144	94.5	5.3	379	11	Q8BLX5	Q8blx5 mus musculus	217	89	5.0	5198	5	Q76518	Q76518 caenorhabdi
145	94.5	5.3	397	11	Q8BFX8	Q8bfx8 mus musculus	218	88.5	5.0	271	12	Q40948	Q40948 kapeei's sa
146	94	5.3	336	6	Q8WNV8	Q8wnv8 felis silve	219	88.5	5.0	315	13	Q9DGL5	Q9dgl5 gallus gall
147	94	5.3	344	11	Q9R067	Q9r067 rattus norv	220	88.5	5.0	325	13	Q8UWL3	Q8uwl3 ictalurus p
148	94	5.3	419	4	Q9QLS5	Q9qll5 homo sapien	221	88.5	5.0	344	13	Q93242	Q93242 gallus gall
149	94	5.3	828	11	Q8C8T7	Q8c8t7 mus musculus	222	88.5	5.0	532	4	Q8WMV6	Q8wmv6 homo sapien
150	93.5	5.3	358	11	Q9R066	Q9r066 rattus norv	223	88.5	5.0	534	4	Q96SA2	Q96sa2 homo sapien
151	93	5.2	316	4	Q9BXR1	Q9bxr1 homo sapien	224	88.5	5.0	554	5	Q9W4R3	Q9w4r3 drosophila
152	93	5.2	339	5	Q9V5T7	Q9v5t7 drosophila	225	88.5	5.0	583	11	Q8CDA5	Q8cdas mus musculus
153	93	5.2	342	13	Q9IB00	Q9ib00 spherooides	226	88.5	5.0	1081	5	Q8T4N8	Q8t4n8 penaeus sem
154	93	5.2	752	13	Q9DGM6	Q9dgm6 gallus gall	227	88	5.0	324	11	Q7TMH2	Q7tmh2 mus musculus
155	93	5.2	793	11	Q70246	Q70246 mus musculus	228	88	5.0	329	6	Q9TFP2	Q9tfp2 canis famil
156	93	5.2	813	11	Q8BQC3	Q8bqc3 mus musculus	229	88	5.0	337	13	Q9IAZA	Q9iaza spherooides
157	93	5.2	1788	13	Q9IAJ0	Q9iaj0 xenopus lae	230	88	5.0	339	13	Q9IB09	Q9ib09 spherooides
158	92.5	5.2	160	11	Q8C239	Q8c239 mus musculus	231	88	5.0	343	11	Q8R4Y0	Q8r4y0 mus musculus
159	92.5	5.2	485	13	Q80LW5	Q80lw5 brachydanio	232	88	5.0	422	17	Q58124	Q58124 pyrococcus
160	92.5	5.2	544	13	Q7ZZ85	Q7zz85 brachydanio	233	88	5.0	457	11	Q61396	Q61396 mus musculus
161	92.5	5.2	760	16	Q8EBB5	Q8ebb5 shewanella	234	88	5.0	530	11	Q80XJ5	Q80xj5 mus musculus
162	92.5	5.2	761	10	Q9C9E3	Q9c9e3 arabidopsis	235	88	5.0	699	11	Q61042	Q61042 mus musculus

236	88	5.0	837	16	Q6G518	Q89518 bifidobacte	309	85.5	4.8	2115	5	Q8IE55	Q8ie55 plasmodium
237	88	5.0	986	13	Q8UV99	Q8uvr9 fugu rubrip	310	85.5	4.8	2491	4	Q96PT5	Q96pts homo sapien
238	88	5.0	1379	5	Q8I3S7	Q8i3s7 plasmodium	311	85.5	4.8	2491	4	Q7Z7G9	Q7z7g9 homo sapien
239	88	5.0	1925	4	Q8IZJ2	Q8izj2 homo sapien	312	85.5	4.8	2588	11	Q88491	Q88491 mus musculus
240	88	5.0	1985	4	Q8Y4D7	Q8y4d7 homo sapien	313	85	4.8	224	3	Q870G0	Q870g0 podospora a
241	88	5.0	3007	4	Q14215	Q14215 homo sapien	314	85	4.8	280	13	Q8UW11	Q8uwl1 ictalurus p
242	87.5	4.9	276	12	Q84861	Q84861 human adeno	315	85	4.8	332	16	Q8EXS1	Q8exsl leptospira
243	87.5	4.9	325	6	Q98822	Q98822 human adeno	316	85	4.8	375	2	Q93GD6	Q93gd6 desulfovibr
244	87.5	4.9	325	6	Q02838	Q02838 sus scrofa	317	85	4.8	379	11	Q8OU19	Q8oul9 mus musculus
245	87.5	4.9	403	11	Q8VEA7	Q8vea7 mus musculus	318	85	4.8	583	6	Q9BH13	Q9bh13 bos taurus
246	87.5	4.9	487	13	Q7T2H2	Q7t2h2 gallus gall	319	85	4.8	684	5	Q21138	Q21138 caenorhabdi
247	87.5	4.9	583	11	Q35112	Q35112 rattus norv	320	85	4.8	709	6	Q9XSJ2	Q9xsj2 sus scrofa
248	87.5	4.9	583	11	Q8R210	Q8r2t0 mus musculus	321	85	4.8	875	11	Q91ZV7	Q91zy7 mus musculus
249	87.5	4.9	652	12	Q89703	Q89703 cassava vei	322	85	4.8	1376	12	Q8AZ23	Q8az23 porcine lym
250	87.5	4.9	1087	13	Q9PUF6	Q9puf6 gallus gall	323	85	4.8	1598	4	Q9P214	Q9p214 homo sapien
251	87.5	4.9	2307	12	Q80IV2	Q80iv2 theiler-lik	324	85	4.8	1723	11	Q8CHB2	Q8chb2 mus musculus
252	87.5	4.9	2340	11	Q64736	Q64736 mus musculus	325	85	4.8	2487	6	Q9N1T0	Q9nlt0 ornithorhyn
253	87.5	4.9	4162	13	Q98918	Q98918 gallus gall	326	84.5	4.8	280	16	Q899D0	Q899d0 clostridium
254	87.5	4.9	4283	11	Q9ERV0	Q9erv0 rattus norv	327	84.5	4.8	303	4	Q7UKJ1	Q7ukj1 homo sapien
255	87.5	4.9	18074	5	Q917U4	Q917u4 drosophila	328	84.5	4.8	355	4	Q7Z3B1	Q7z3b1 homo sapien
256	87	4.9	229	11	Q9R121	Q9r121 rattus norv	329	84.5	4.8	394	11	Q9D0G8	Q9d0g8 mus musculus
257	87	4.9	291	11	Q8C6C3	Q8c6c3 mus musculus	330	84.5	4.8	656	10	Q04533	Q04533 arabidopsis
258	87	4.9	326	11	Q8CI91	Q8ci91 mus musculus	331	84.5	4.8	798	5	Q96K66	Q96k66 dictyosteli
259	87	4.9	341	11	Q81333	Q81333 mus musculus	332	84.5	4.8	840	16	Q7VQ12	Q7vq12 candidatus
260	87	4.9	403	11	Q9CYD6	Q9cyd6 mus musculus	333	84.5	4.8	1164	17	Q8PX58	Q8px58 methanosarc
261	87	4.9	415	11	Q8C6X8	Q8c6x8 mus musculus	334	84.5	4.8	1608	17	Q8PVI0	Q8pvi0 methanosarc
262	87	4.9	491	11	Q8BQZ8	Q8bqz8 mus musculus	335	84.5	4.8	4311	6	Q7YQK5	Q7ygk5 canis famil
263	87	4.9	514	11	Q8BH18	Q8bh18 mus musculus	336	84	4.7	262	13	Q9PTR7	Q9ptr7 spherooides
264	87	4.9	521	6	Q46551	Q46551 oryctolagus	337	84	4.7	333	13	Q9IB04	Q9ib04 spherooides
265	87	4.9	522	16	Q8F7F1	Q8f7f1 leptospira	338	84	4.7	343	11	Q8BYS4	Q8by54 mus musculus
266	87	4.9	873	11	Q8CD46	Q8cd46 mus musculus	339	84	4.7	403	16	Q8ENX5	Q8enx5 oceanobacil
267	87	4.9	1501	11	Q7T1T7	Q7t1t7 mus musculus	340	84	4.7	556	13	Q7ZZU8	Q7zzu8 brachydanio
268	87	4.9	1904	11	Q64699	Q64699 mus musculus	341	84	4.7	593	3	Q8NKB1	Q8nkb1 emericella
269	87	4.9	2673	4	Q965C3	Q965c3 homo sapien	342	84	4.7	775	6	Q97754	Q97754 oryctolagus
270	86.5	4.9	293	13	Q9AXN8	Q9axn8 cyprinus ca	343	84	4.7	800	10	Q8H329	Q8h329 oryza sativ
271	86.5	4.9	313	11	Q35531	Q35531 rattus norv	344	84	4.7	810	5	Q8T3U2	Q8t3j2 drosophila
272	86.5	4.9	324	13	Q9IAY9	Q9iay9 spherooides	345	84	4.7	811	5	Q9VK54	Q9vk54 drosophila
273	86.5	4.9	354	4	Q8NAQ3	Q8naq3 homo sapien	346	84	4.7	812	5	Q8M257	Q8mz57 drosophila
274	86.5	4.9	474	6	P79355	P79355 felis silve	347	84	4.7	851	17	Q9UX76	Q9ux76 sulfolobus
275	86.5	4.9	528	16	Q9RTP5	Q9rtp5 deinococcus	348	84	4.7	880	5	P91643	P91643 drosophila
276	86.5	4.9	650	16	Q88BN9	Q88bn9 pseudomonas	349	84	4.7	992	10	Q7XTP4	Q7xtp4 oryza sativ
277	86.5	4.9	846	11	Q810C0	Q810c0 mus musculus	350	84	4.7	1062	12	Q997A4	Q997a4 american pl
278	86	4.9	259	4	Q9Y5B2	Q9y5b2 homo sapien	351	84	4.7	1193	5	Q9VQW1	Q9vgw1 drosophila
279	86	4.9	280	13	Q8UW11	Q8uwl1 ictalurus p	352	84	4.7	1499	13	Q90815	Q90815 gallus gall
280	86	4.9	339	13	Q9IAZ1	Q9iaz1 spherooides	353	83.5	4.7	284	6	Q9GL33	Q9gl33 bos taurus
281	86	4.9	354	12	Q98VN1	Q98vn1 human herpe	354	83.5	4.7	289	11	Q8K3J3	Q8k3j3 meriones un
282	86	4.9	428	4	Q9BRW2	Q9brw2 homo sapien	355	83.5	4.7	315	17	Q50082	Q50082 pyrococcus
283	86	4.9	486	16	Q82N16	Q82ni6 streptomyce	356	83.5	4.7	392	5	Q76708	Q76708 caenorhabdi
284	86	4.9	487	16	Q82MT3	Q82mt3 streptomyce	357	83.5	4.7	408	11	Q91WP1	Q91wp1 mus musculus
285	86	4.9	545	5	Q9VCT4	Q9vct4 drosophila	358	83.5	4.7	408	11	Q8BVF6	Q8bvf6 mus musculus
286	86	4.9	687	10	Q9MAJ5	Q9maj5 arabidopsis	359	83.5	4.7	408	11	Q8K094	Q8k094 mus musculus
287	86	4.9	731	6	Q8SPI6	Q8spi6 macropus eu	360	83.5	4.7	515	4	Q96R50	Q96re0 homo sapien
288	86	4.9	885	10	Q8L3K3	Q8l3r3 arabidopsis	361	83.5	4.7	515	4	Q96PJ5	Q96pj5 homo sapien
289	86	4.9	885	10	Q8L3X7	Q8l3y7 arabidopsis	362	83.5	4.7	528	5	P91670	P91670 drosophila
290	86	4.9	885	10	Q81401	Q81401 arabidopsis	363	83.5	4.7	577	16	Q8IH34	Q8ih34 bacillus ce
291	86	4.9	885	10	Q8LGP8	Q8lgp8 arabidopsis	364	83.5	4.7	646	16	Q899V4	Q899v4 clostridium
292	86	4.9	1187	13	Q98TF0	Q98tf0 cyprinus ca	365	83.5	4.7	1059	13	Q9D549	Q9de49 brachydanio
293	86	4.9	1327	4	Q15070	Q15070 homo sapien	366	83.5	4.7	1463	11	Q55124	Q55124 mus musculus
294	86	4.9	18412	13	Q7Z251	Q7zz61 brachydanio	367	83.5	4.7	1501	11	Q9QW00	Q9qw00 rattus sp.
295	85.5	4.8	324	4	Q9UPK9	Q9upk9 homo sapien	368	83.5	4.7	1556	16	Q83NF7	Q83nf7 tropheryma
296	85.5	4.8	326	4	Q9UPK8	Q9upk8 homo sapien	369	83.5	4.7	1802	12	Q9J5C2	Q9j5c2 fowlpox vir
297	85.5	4.8	333	4	Q75238	Q75238 homo sapien	370	83.5	4.7	1863	11	Q64605	Q64605 rattus norv
298	85.5	4.8	335	4	Q75237	Q75237 homo sapien	371	83	4.7	151	6	Q7VS89	Q7vs89 sus scrofa
299	85.5	4.8	393	11	Q7TNZ6	Q7tnz6 rattus norv	372	83	4.7	231	4	Q8WYV6	Q8wyv6 homo sapien
300	85.5	4.8	650	4	Q8NAB4	Q8na84 homo sapien	373	83	4.7	234	11	Q61401	Q61401 mus musculus
301	85.5	4.8	657	2	Q93D79	Q93d79 bacillus th	374	83	4.7	273	4	Q9NQD3	Q9ngd3 homo sapien
302	85.5	4.8	789	2	Q45793	Q45793 bacillus th	375	83	4.7	281	11	Q8CJEB	Q8cje8 mesocricetu
303	85.5	4.8	789	2	Q69270	Q69270 bacillus th	376	83	4.7	319	11	Q9JKA5	Q9jka5 mus musculus
304	85.5	4.8	789	2	Q45792	Q45792 bacillus th	377	83	4.7	339	13	Q9IAZ2	Q9iaz2 spherooides
305	85.5	4.8	789	2	Q938Z1	Q938z1 bacillus th	378	83	4.7	369	2	Q93EWS	Q93ew5 desulfovibr
306	85.5	4.8	1101	10	Q9FWL8	Q9fwl8 oryza sativ	379	83	4.7	373	17	Q8TU74	Q8tu74 methanosarc
307	85.5	4.8	1101	10	Q7XDJ5	Q7xdj5 oryza sativ	380	83	4.7	401	6	Q08835	Q08835 cercopithec
308	85.5	4.8	1354	5	Q9VIC7	Q9vic7 drosophila	381	83	4.7	437	13	Q90W14	Q90w14 gallus gall

382	83	4.7	514	4	Q9H0C3	Q9h0c3 homo sapien	455	81.5	4.6	473	16	Q8ZQD1	Q8zqd1 salmonella
383	83	4.7	538	13	Q9DFU0	Q9dfu0 sparus aura	456	81.5	4.6	502	2	Q842D1	Q842d1 escherichia
384	83	4.7	577	11	Q9D221	Q9d221 mus musculus	457	81.5	4.6	504	4	Q8N441	Q8n441 homo sapien
385	83	4.7	885	10	Q8LQ00	Q8lq00 arabidopsis	458	81.5	4.6	504	4	Q9H4D7	Q9h4d7 homo sapien
386	83	4.7	885	10	Q8LQ00	Q8lq00 arabidopsis	459	81.5	4.6	524	2	Q901D2	Q901d2 shigella so
387	83	4.7	885	10	Q8LQ00	Q8lq00 arabidopsis	460	81.5	4.6	606	5	Q9VMN6	Q9vmn6 drosophila
388	83	4.7	925	5	Q9U4E4	Q9u4e4 caenorhabdi	461	81.5	4.6	677	16	Q8A3Q5	Q8a3q5 bacteroides
389	83	4.7	925	5	Q9U4E4	Q9u4e4 caenorhabdi	462	81.5	4.6	708	10	Q9M1P4	Q9m1p4 arabidopsis
390	83	4.7	925	5	Q9U4E4	Q9u4e4 caenorhabdi	463	81.5	4.6	779	16	Q8AAG1	Q8aag1 bacteroides
391	83	4.7	925	5	Q9U4E4	Q9u4e4 caenorhabdi	464	81.5	4.6	824	16	Q8A3C4	Q8a3c4 bacteroides
392	83	4.7	1106	5	Q8IBR5	Q8ibr5 plasmodium	465	81.5	4.6	824	16	Q8A3C4	Q8a3c4 bacteroides
393	83	4.7	2421	3	Q95MJ1	Q95mj1 lemur catta	466	81.5	4.6	968	5	Q9VR40	Q9vr40 drosophila
394	83	4.7	2489	3	Q95MJ1	Q95mj1 lemur catta	467	81.5	4.6	968	5	Q9VR40	Q9vr40 drosophila
395	82.5	4.7	155	4	Q96P81	Q96p81 homo sapien	468	81.5	4.6	1187	13	Q93284	Q93284 fugu rubrip
396	82.5	4.7	155	4	Q96P81	Q96p81 homo sapien	469	81.5	4.6	1187	13	Q93284	Q93284 fugu rubrip
397	82.5	4.7	230	13	Q8UW76	Q8uw76 brachydanio	470	81.5	4.6	1194	3	Q93962	Q93962 gliomus vers
398	82.5	4.7	244	6	Q7YS40	Q7ys40 sus scrofa	471	81.5	4.6	1194	3	Q93962	Q93962 gliomus vers
399	82.5	4.7	270	4	Q9H564	Q9h564 homo sapien	472	81.5	4.6	1214	4	Q75054	Q75054 mus musculus
400	82.5	4.7	319	11	Q922D5	Q922d5 mus musculus	473	81.5	4.6	1214	4	Q75054	Q75054 mus musculus
401	82.5	4.7	330	11	P97269	P97269 cavia porce	474	81.5	4.6	1596	4	Q9HCL6	Q9hcl6 homo sapien
402	82.5	4.7	373	10	Q9SSH0	Q9ssh0 arabidopsis	475	81.5	4.6	2212	4	Q8NHN3	Q8nhn3 homo sapien
403	82.5	4.7	378	10	Q8L4Y2	Q8l4y2 arabidopsis	476	81.5	4.6	2284	5	Q8ISY7	Q8isy7 plasmodium
404	82.5	4.7	393	10	Q9C9F8	Q9c9f8 arabidopsis	477	81	4.6	2284	5	Q8ISY7	Q8isy7 plasmodium
405	82.5	4.7	446	3	Q8NK03	Q8nk03 emericella	478	81	4.6	6620	4	Q96AA2	Q96aa2 homo sapien
406	82.5	4.7	462	10	Q8LBP4	Q8lbp4 arabidopsis	479	81	4.6	6620	4	Q96AA2	Q96aa2 homo sapien
407	82.5	4.7	576	17	Q8TQK0	Q8tk0 methanosarc	480	81	4.6	149	5	Q86L22	Q86l22 dictyosteli
408	82.5	4.7	840	2	Q9VHG1	Q9vhl1 drosophila	481	81	4.6	151	6	Q867B8	Q867b8 sus scrofa
409	82.5	4.7	840	2	Q9VHG1	Q9vhl1 drosophila	482	81	4.6	151	6	Q867B8	Q867b8 sus scrofa
410	82.5	4.7	994	5	Q9Q522	Q9q522 mus musculus	483	81	4.6	252	4	Q95781	Q95781 homo sapien
411	82.5	4.7	1028	4	Q9Q522	Q9q522 mus musculus	484	81	4.6	252	4	Q95781	Q95781 homo sapien
412	82.5	4.7	1241	16	Q83GQ1	Q83gq1 tropheryma	485	81	4.6	272	7	Q86LJ5	Q86lj5 equus caball
413	82.5	4.7	1319	5	Q9BJF3	Q9bjf3 oxytricha t	486	81	4.6	291	11	Q8CD40	Q8cd40 mus musculus
414	82.5	4.7	4256	6	Q8MIF3	Q8mif3 canis famil	487	81	4.6	326	13	Q9IAY7	Q9iay7 spherooides
415	82.5	4.7	4650	4	Q15598	Q15598 homo sapien	488	81	4.6	326	13	Q9IAY7	Q9iay7 spherooides
416	82.5	4.7	2626	4	Q8WZB3	Q8wzb3 homo sapien	489	81	4.6	338	4	Q8IIV4	Q8iiv4 homo sapien
417	82.5	4.7	2626	4	Q8WZB3	Q8wzb3 homo sapien	490	81	4.6	338	4	Q8IIV4	Q8iiv4 homo sapien
418	82.5	4.7	34350	4	Q8WZ42	Q8wz42 homo sapien	491	81	4.6	374	10	Q43741	Q43741 bromheadia
419	82	4.6	151	6	Q7YS88	Q7ys88 sus scrofa	492	81	4.6	423	5	Q9UAG6	Q9uag6 dictyosteli
420	82	4.6	184	16	Q7VM71	Q7vm71 haemophilus	493	81	4.6	438	11	Q920C3	Q920c3 mus musculus
421	82	4.6	308	6	Q9SK99	Q9sk99 macaca fasc	494	81	4.6	438	11	Q920C3	Q920c3 mus musculus
422	82	4.6	324	4	Q8NBY8	Q8nby8 homo sapien	495	81	4.6	451	16	Q8DDA0	Q8dda0 vibrio vuln
423	82	4.6	326	4	Q8NBY8	Q8nby8 homo sapien	496	81	4.6	451	16	Q8DDA0	Q8dda0 vibrio vuln
424	82	4.6	327	4	Q96IQ7	Q96iq7 homo sapien	497	81	4.6	507	5	Q9U319	Q9u319 caenorhabdi
425	82	4.6	331	13	Q9IB01	Q9ib01 spherooides	498	81	4.6	521	6	Q46634	Q46634 canis famil
426	82	4.6	409	16	Q814W1	Q814w1 bacillus ce	499	80.5	4.5	624	10	Q94AX9	Q94ax9 arabidopsis
427	82	4.6	412	6	Q8HY14	Q8hy14 ocyctolagus	500	80.5	4.5	624	10	Q94AX9	Q94ax9 arabidopsis
428	82	4.6	444	10	Q8S9I7	Q8s9i7 arabidopsis	501	80.5	4.5	769	16	Q7Y231	Q7y231 mus musculus
429	82	4.6	449	3	P78721	P78721 orpinomyces	502	80.5	4.5	769	16	Q7Y231	Q7y231 mus musculus
430	82	4.6	587	13	Q9IAA1	Q9iaa1 carassius a	503	80.5	4.5	937	16	Q8G4P3	Q8g4p3 bifidobacte
431	82	4.6	634	3	Q9P8L1	Q9p8l1 cryptococcu	504	80.5	4.5	937	16	Q8G4P3	Q8g4p3 bifidobacte
432	82	4.6	648	11	Q9EPF1	Q9epf1 mus musculu	505	80.5	4.5	1196	13	Q98TF1	Q98tf1 cyprinus ca
433	82	4.6	709	6	Q8XSJ1	Q8xsl1 bos taurus	506	80.5	4.5	1220	3	Q9P3A8	Q9p3a8 schizosacch
434	82	4.6	709	11	Q88702	Q88702 rattus norv	507	80.5	4.5	1220	3	Q9P3A8	Q9p3a8 schizosacch
435	82	4.6	737	11	Q70376	Q70376 rattus norv	508	80.5	4.5	261	13	Q9U6V1	Q9umt1 homo sapien
436	82	4.6	757	11	Q70482	Q70482 rattus norv	509	80.5	4.5	270	4	Q9U6V1	Q9umt1 homo sapien
437	82	4.6	785	11	Q9QZ29	Q9qzf9 rattus norv	510	80.5	4.5	290	16	Q8CRR9	Q8crr9 staphylococ
438	82	4.6	795	4	Q8ND69	Q8nd69 homo sapien	511	80.5	4.5	371	16	Q816Y2	Q816y2 bacillus ce
439	82	4.6	890	4	Q8GVE3	Q8gve3 mus musculu	512	80.5	4.5	371	16	Q816Y2	Q816y2 bacillus ce
440	82	4.6	1038	11	Q8CH3A	Q8cha3 mus musculu	513	80.5	4.5	376	10	Q94B08	Q94b08 arabidopsis
441	82	4.6	1166	11	Q80VFO	Q80vfo mus musculu	514	80.5	4.5	376	10	Q94B08	Q94b08 arabidopsis
442	82	4.6	2136	10	Q8RYW8	Q8ryw8 oryza sativ	515	80.5	4.5	376	10	Q23195	Q23195 arabidopsis
443	82	4.6	2940	5	Q8IHP9	Q8ihp9 plasmodium	516	80.5	4.5	388	11	Q8R464	Q8r464 mus musculu
444	82	4.6	3173	16	Q882M6	Q882m6 pseudomonas	517	80.5	4.5	472	11	Q811T8	Q811t8 mus musculu
445	82	4.6	5636	4	Q96RW7	Q96rw7 homo sapien	518	80.5	4.5	472	11	Q811T8	Q811t8 mus musculu
446	81.5	4.6	275	13	Q8AVV1	Q8avv1 xenopus lae	519	80.5	4.5	546	11	Q99NB3	Q99nb3 mus musculu
447	81.5	4.6	329	13	Q9IAV6	Q9iaav6 spherooides	520	80.5	4.5	546	11	Q99NB3	Q99nb3 mus musculu
448	81.5	4.6	336	13	Q90Z89	Q90z89 brachydanio	521	80.5	4.5	556	16	Q8DEW4	Q8dew4 vibrio vuln
449	81.5	4.6	340	13	Q9IAZ6	Q9iaaz6 spherooides	522	80.5	4.5	564	13	Q7ZU00	Q7zu00 brachydanio
450	81.5	4.6	352	4	Q15403	Q15403 homo sapien	523	80.5	4.5	602	4	Q86YU9	Q86y9 homo sapien
451	81.5	4.6	352	4	Q82666	Q82666 homo sapien	524	80.5	4.5	662	4	Q60926	Q60926 homo sapien
452	81.5	4.6	355	10	Q65493	Q65493 arabidopsis	525	80.5	4.5	707	10	Q7XNT7	Q7xnt7 oryza sativ
453	81.5	4.6	411	4	Q15228	Q15228 homo sapien	526	80.5	4.5	721	3	Q13479	Q13479 aspergillus
454	81.5	4.6	438	13	Q7T0Z8	Q7t0z8 xenopus lae	527	80.5	4.5	739	6	Q865F2	Q865f2 ocyctolagus
										789	2	Q8RS25	Q8rsz5 bacillus th
										823	10	Q93594	Q93594 chlamydomon
										932	11	Q7TQ14	Q7tq14 rattus norv
										976	13	Q8JFR5	Q8jfr5 brachydanio
										976	13	Q9W755	Q9w755 brachydanio
										1146	13	Q9I8V6	Q9i8v6 gallus gall
										1202	11	Q80U33	Q80u33 mus musculu
										1465	4	Q7Z3Y2	Q7z3y2 homo sapien

528	80.5	4.5	2253	12	Q8JV20	Q8jv20 ljungan vir	601	79	4.5	524	9	Q8LTK1	Q8ltk1 lactococcus
529	80.5	4.5	2358	6	Q85MJ2	Q85mj2 macrosporus ru	602	79	4.5	526	11	Q80WA6	Q80wa6 mus musculus
530	80.5	4.5	2898	3	Q872P1	Q872p1 neurospora	603	79	4.5	584	4	Q9Y3Y8	Q9y3y8 homo sapien
531	80.5	4.5	3337	5	Q9TWY4	Q9twy4 caenorhabdi	604	79	4.5	590	3	Q9P4U4	Q9p4u4 candida tro
532	80.5	4.5	8081	5	Q7Z120	Q7z120 caenorhabdi	605	79	4.5	611	13	Q9IBP6	Q9ibf6 xenopus lae
533	80	4.5	184	4	Q8WV18	Q8wv18 homo sapien	606	79	4.5	611	13	Q9PT10	Q9pt10 xenopus lae
534	80	4.5	227	4	Q9UKJ0	Q9ukj0 mus musculus	607	79	4.5	619	10	Q9ASG9	Q9asg9 oryza sativ
535	80	4.5	235	11	Q99M11	Q99m11 mus musculus	608	79	4.5	657	16	P73359	P73359 synechocyst
536	80	4.5	303	13	Q7T114	Q7t114 brachydanio	609	79	4.5	711	11	Q80Y89	Q80y89 mus musculus
537	80	4.5	337	13	Q8WV29	Q8wv29 brachydanio	610	79	4.5	778	5	Q9N4B1	Q9n4b1 caenorhabdi
538	80	4.5	341	11	Q8BLK3	Q8blk3 mus musculus	611	79	4.5	783	11	Q8L1H8	Q8l1h8 mus musculus
539	80	4.5	343	16	Q8X5J1	Q8x5j1 escherichia	612	79	4.5	785	11	Q7TNP4	Q7tnp4 mus musculus
540	80	4.5	365	13	Q8AXL6	Q8axl6 oncorhynchus	613	79	4.5	807	17	Q8PTE2	Q8pte2 methanosarc
541	80	4.5	436	4	Q9N563	Q9n563 homo sapien	614	79	4.5	903	5	Q19372	Q19372 caenorhabdi
542	80	4.5	440	6	Q8MK36	Q8mk36 macaca mula	615	79	4.5	920	10	Q8GZA0	Q8gza0 arabidopsis
543	80	4.5	509	11	Q920C2	Q920c2 mus musculus	616	79	4.5	1092	11	Q8BP24	Q8bp24 mus musculus
544	80	4.5	516	4	Q81WX2	Q81wx2 homo sapien	617	79	4.5	1104	11	Q9PKX7	Q9fkr7 arabidopsis
545	80	4.5	529	11	Q91V87	Q91v87 mus musculus	618	79	4.5	1264	5	P91767	P91767 manduca sex
546	80	4.5	624	10	Q8LG08	Q8lg08 arabidopsis	619	79	4.5	1728	11	Q80TC7	Q80tc7 mus musculus
547	80	4.5	627	5	Q9VUL0	Q9vul0 drosophila	620	79	4.5	1887	11	Q9QM67	Q9qm67 rattus sp.
548	80	4.5	633	13	Q7SXC1	Q7sxc1 brachydanio	621	79	4.5	4010	11	Q80T14	Q80t14 mus musculus
549	80	4.5	637	3	Q9P8P2	Q9p8p2 cryptococcus	622	78.5	4.4	305	6	Q9BE65	Q9be65 macaca fasc
550	80	4.5	681	5	Q86J56	Q86j56 dictyosteli	623	78.5	4.4	318	13	Q91664	Q91664 xenopus lae
551	80	4.5	913	11	Q9QYM7	Q9qym7 cricetus	624	78.5	4.4	388	4	Q8NFZ8	Q8nfz8 homo sapien
552	80	4.5	1005	13	P79921	P79921 xenopus lae	625	78.5	4.4	431	3	Q8X022	Q8x022 neurospora
553	80	4.5	1192	16	Q81Y28	Q81y28 bacillus an	626	78.5	4.4	452	5	O76773	O76773 lucilia cup
554	80	4.5	1310	5	Q81714	Q81714 caenorhabdi	627	78.5	4.4	459	10	Q9SS39	Q9ss39 arabidopsis
555	80	4.5	1431	16	Q8EW23	Q8ew23 mycoplasma	628	78.5	4.4	471	11	Q9DAV5	Q9davs mus musculus
556	80	4.5	1925	12	Q9YRB3	Q9yrb3 nudaurelia	629	78.5	4.4	537	2	Q93E12	Q93e12 rhizobium l
557	80	4.5	2456	5	Q81715	Q81715 caenorhabdi	630	78.5	4.4	539	10	O04252	O04252 arabidopsis
558	79.5	4.5	151	11	Q8C2T1	Q8c2t1 mus musculus	631	78.5	4.4	556	10	Q8LA44	Q8la44 arabidopsis
559	79.5	4.5	244	6	Q8SQB6	Q8sqb6 sus scrofa	632	78.5	4.4	629	10	Q8LA44	Q8la44 arabidopsis
560	79.5	4.5	289	17	Q97XZ7	Q97xz7 sulfobacil	633	78.5	4.4	638	10	Q9LF94	Q9lfs4 arabidopsis
561	79.5	4.5	399	16	Q8EMV2	Q8emv2 oceanobacil	634	78.5	4.4	651	16	Q88BU0	Q88bu0 pseudomonas
562	79.5	4.5	400	16	Q8ZHN7	Q8zhn7 yersinia pe	635	78.5	4.4	810	4	Q9Y5C8	Q9y5c8 homo sapien
563	79.5	4.5	401	13	Q9S534	Q9s534 xenopus lae	636	78.5	4.4	844	3	Q875H9	Q875h9 candida alb
564	79.5	4.5	446	16	Q8S985	Q8s985 streptomyce	637	78.5	4.4	888	13	Q7ZWM9	Q7zwm9 xenopus lae
565	79.5	4.5	474	13	Q7ZU39	Q7zu39 brachydanio	638	78.5	4.4	927	4	Q9Y5G3	Q9y5g3 homo sapien
566	79.5	4.5	520	2	Q8GDL8	Q8gd18 photorhabdu	639	78.5	4.4	1038	16	Q8YSN0	Q8ysn0 anabaena sp
567	79.5	4.5	641	5	Q86SD2	Q86sd2 ciona intes	640	78.5	4.4	1465	10	Q8GYU3	Q8gyu3 arabidopsis
568	79.5	4.5	821	11	Q8C756	Q8c756 mus musculus	641	78.5	4.4	1468	10	Q9SVZ1	Q9svz1 arabidopsis
569	79.5	4.5	845	11	Q91YX0	Q91yxo mus musculus	642	78.5	4.4	1788	4	O60612	O60612 homo sapien
570	79.5	4.5	961	11	Q80W87	Q80w87 rattus norv	643	78.5	4.4	1915	2	Q9RPLE0	Q9rpl0 acetivibrio
571	79.5	4.5	1162	4	Q75921	Q75921 homo sapien	644	78	4.4	236	4	Q8NEJ1	Q8nej1 homo sapien
572	79.5	4.5	1162	4	Q9UNY4	Q9uny4 homo sapien	645	78	4.4	257	16	Q97I62	Q97i62 clostridium
573	79.5	4.5	1171	11	Q8CGB2	Q8cgb2 mus musculus	646	78	4.4	272	11	Q8R1N5	Q8r1n5 mus musculus
574	79.5	4.5	1171	11	Q80YQ1	Q80yq1 mus musculus	647	78	4.4	287	4	Q13984	Q13984 homo sapien
575	79.5	4.5	1342	5	Q9GPP6	Q9gpp6 drosophila	648	78	4.4	304	4	O43754	O43754 homo sapien
576	79.5	4.5	1342	5	Q9VPZ7	Q9vpz7 drosophila	649	78	4.4	313	13	O57596	O57596 gallus gall
577	79.5	4.5	1838	11	Q88207	Q88207 mus musculus	650	78	4.4	375	12	Q65280	Q65280 african swi
578	79.5	4.5	2253	12	Q8JY21	Q8jy21 ljungan vir	651	78	4.4	399	4	Q9Y279	Q9y279 homo sapien
579	79.5	4.5	2256	12	Q8JY19	Q8jy19 ljungan vir	652	78	4.4	402	11	O35444	O35444 mus musculus
580	79.5	4.5	2558	5	Q9GRL9	Q9grl9 leishmania	653	78	4.4	412	16	Q8G6P7	Q8g6p7 bifidobacte
581	79.5	4.5	2706	5	Q97292	Q97292 plasmodium	654	78	4.4	423	2	Q9RBI2	Q9rb12 acinetobact
582	79	4.5	158	4	Q15229	Q15229 homo sapien	655	78	4.4	452	16	Q7VQM5	Q7vqm5 candidata
583	79	4.5	210	16	Q9AC09	Q9ac09 caulobacter	656	78	4.4	491	5	Q9VKX6	Q9vkk6 drosophila
584	79	4.5	222	6	Q8MK98	Q8mk98 macroscelid	657	78	4.4	604	3	O74491	O74491 schizosacch
585	79	4.5	226	5	Q8GP32	Q8gp32 drosophila	658	78	4.4	606	11	Q9ESS7	Q9eas7 mus musculus
586	79	4.5	244	16	Q927X2	Q927x2 listeria in	659	78	4.4	608	16	Q8YCV9	Q8ycv9 brucella me
587	79	4.5	271	7	Q9S161	Q9s161 gadus morhu	660	78	4.4	608	16	Q8FV66	Q8fv66 brucella su
588	79	4.5	323	4	Q8NDD2	Q8ndd2 homo sapien	661	78	4.4	634	3	Q8X0Z4	Q8x0z4 cryptococcu
589	79	4.5	342	6	Q8MK29	Q8mk29 macaca mula	662	78	4.4	634	3	Q96WX0	Q96wx0 cryptococcu
590	79	4.5	406	11	Q8BPP7	Q8bpp7 mus musculus	663	78	4.4	648	11	Q8R2Y2	Q8r2y2 mus musculus
591	79	4.5	410	16	Q81JPS	Q81jp5 bacillus an	664	78	4.4	706	11	Q8BM11	Q8bm11 mus musculus
592	79	4.5	429	11	Q8BFS1	Q8bfs1 mus musculus	665	78	4.4	836	9	O48483	O48483 bacteriopho
593	79	4.5	440	6	Q8MK37	Q8mk37 macaca mula	666	78	4.4	865	15	Q8Q7H7	Q8q7h7 human immun
594	79	4.5	446	13	P79762	P79762 gallus gall	667	78	4.4	905	3	O13955	O13955 schizosacch
595	79	4.5	446	13	Q9PWF8	Q9pwf8 gallus gall	668	78	4.4	1009	13	Q93250	Q93250 xenopus lae
596	79	4.5	464	16	Q88KY8	Q88ky8 pseudomonas	669	78	4.4	1016	16	O8A4W1	O8a4w1 bacteroides
597	79	4.5	479	16	Q9K6X5	Q9k6x5 bacillus ha	670	78	4.4	1147	13	Q9DDK1	Q9ddk1 meleagris g
598	79	4.5	490	4	Q8WU21	Q8wuz1 homo sapien	671	78	4.4	1924	3	Q7ZDU6	Q7zdu6 aspergillus
599	79	4.5	491	10	Q8GZP5	Q8gzp5 lycopersico	672	78	4.4	3722	2	P94873	P94873 lyobacter
600	79	4.5	517	4	O76021	O76021 homo sapien	673	77.5	4.4	117	13	Q7Z267	Q7zz67 brachydanio

674 77.5 4.4 128 4 Q86UW2 Q86uw2 homo sapien
 675 77.5 4.4 172 5 Q19627 Q19627 caenorhabdi
 676 77.5 4.4 186 5 Q8MV99 Q8mv99 ixodes scap
 677 77.5 4.4 214 16 Q9SVY1 Q9svy1 staphylococ
 678 77.5 4.4 258 4 Q9H563 Q9h563 homo sapien
 679 77.5 4.4 284 4 Q9NX42 Q9nx42 homo sapien
 680 77.5 4.4 294 11 Q8K125 Q8k125 mus musculus
 681 77.5 4.4 300 11 Q9JHY1 Q9jhy1 rattus norv
 682 77.5 4.4 324 10 Q940M5 Q940m5 arabidopsis
 683 77.5 4.4 326 13 Q9IAZ3 Q9iaz3 spherooides
 684 77.5 4.4 345 8 Q9G9W4 Q9g9w4 teleogrylli
 685 77.5 4.4 345 8 Q9ADW3 Q9adw3 teleogrylli
 686 77.5 4.4 351 2 Q9ADX7 Q9adx7 agrobacteri
 687 77.5 4.4 356 13 Q9AXL7 Q9axl7 oncorhynchus
 688 77.5 4.4 360 16 Q7VAZ7 Q7vaz7 prochloroco
 689 77.5 4.4 371 16 Q81KQ7 Q81kq7 bacillus an
 690 77.5 4.4 425 3 Q96VU0 Q96vu0 amanita mus
 691 77.5 4.4 428 16 Q8F7J7 Q8f7j7 leptospira
 692 77.5 4.4 433 11 Q55054 Q55054 mus musculus
 693 77.5 4.4 460 5 Q7YTAB Q7yta8 bombyx mori
 694 77.5 4.4 476 11 Q9CU34 Q9cu34 mus musculus
 695 77.5 4.4 536 16 Q7UZH7 Q7uzh7 prochloroco
 696 77.5 4.4 539 10 Q9FX24 Q9fx24 arabidopsis
 697 77.5 4.4 589 10 Q9RZH3 Q9rzh3 oryza sativ
 698 77.5 4.4 591 16 Q91LK8 Q91lk8 pseudomonas
 699 77.5 4.4 717 16 Q8U7P9 Q8u7p9 agrobacteri
 700 77.5 4.4 735 10 Q9FG24 Q9fg24 arabidopsis

ALIGNMENTS

RESULT 1

Q9NQ25 PRELIMINARY; PRT; 335 AA.
 ID Q9NQ25
 AC Q9NQ25; 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE BA04F10.4 (Novel LY9 (lymphocyte antigen 9) like protein) (NK cell
 DE receptor) (Membrane protein FOAP-12) (CD2-like receptor activating
 DE cytotoxic cells).
 GN BA04F10.4 OR CSI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bates K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Boles K.S., Mathew P.A. Sr.;
 RL "Cloning of a new member of the CD2 subset of receptors expressed on
 RL NK cells";
 RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Macrophage;
 RC Fujii Y., Takayama K., Tsuritani K., Yajima Y., Amemiya T., Ukai Y.,
 RA Naito K., Kawaguchi A.;
 RL "Homo sapiens mRNA for FOAP-12 protein, complete cds";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bouchon A., Cella M., Grierson H.L., Cohen J.I., Colonna M.;
 RL "Cutting Edge: Activation of NK Cell-Mediated Cytotoxicity by a SAP-
 RL Independent Receptor of the CD2 Family.";
 RL J. Immunol. 167:0-0(2001).
 DR EMBL; AL121985; CAC00579.1; --
 DR EMBL; AF291815; AAK11549.1; --
 DR EMBL; AB027233; BAB61022.1; --

DR EMBL; AF390894; AAL26989.1; --
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR003599; IG-like.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Receptor.
 SQ SEQUENCE 335 AA; 37421 MW; D09ABBCFF74BE8D4 CRC64;
 Query Match 100.0%; Score 1772; DB 4; Length 335;
 Best Local Similarity 100.0%; Pred. No. 6.5e-159;
 Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTPL 60
 DB 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTPL 60
 QY 61 VTIOPEGGTIIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYGVYSSSIQQPSTQY 120
 DB 61 VTIOPEGGTIIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYGVYSSSIQQPSTQY 120
 QY 121 VLHYEHLSPKVTMGLOSNGKTCVNTLTCMBHEBEDVIYTWKALQQAANESHGSI 180
 DB 121 VLHYEHLSPKVTMGLOSNGKTCVNTLTCMBHEGEDVIYTWKALQQAANESHGSI 180
 QY 181 PISRWGESDMTFCVARNPVSRNFPSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
 DB 181 PISRWGESDMTFCVARNPVSRNFPSPILARKLCEGAADDPDSSMWLLCLLLVPLLSL 240
 QY 241 FVLGLFWLFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
 DB 241 FVLGLFWLFLKRRQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA 300
 QY 301 NTVYSTVEIPKKNPHSLTMDPTPLFAYENVI 335
 DB 301 NTVYSTVEIPKKNPHSLTMDPTPLFAYENVI 335

RESULT 2

Q9NY08 PRELIMINARY; PRT; 335 AA.
 ID Q9NY08
 AC Q9NY08; 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE 19A protein.
 GN 19A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
 RL "An early response gene that encodes an immunoglobulin superfamily
 RL member with structural similarity to CD2";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ276429; CAB81950.2; --
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 SQ SEQUENCE 335 AA; 37403 MW; BB758E505CA4DD5 CRC64;
 Query Match 99.8%; Score 1769; DB 4; Length 335;
 Best Local Similarity 99.7%; Pred. No. 1.2e-158;
 Matches 334; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTPL 60
 DB 1 MAGSPCTCLTIYILWQLTGSAAAGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTPL 60
 QY 61 VTIOPEGGTIIIVTQNRNRERVDPPDGGYSLKSLKKNDSGIYVYGVYSSSIQQPSTQY 120

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Db 61 VTIQEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYGIIYSSSLQQPSTQBY 120
121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 3
Q9NY23
ID Q9NY23 PRELIMINARY; PRT; 328 AA.
AC Q9NY23;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 19A24 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Murphy J.J., Norton J.D., Hobby P., Sutton B.J.;
RT "An early response gene that encodes an immunoglobulin superfamily
RL member with structural similarity to CD2."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271869; CAB76561.1; -
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 328 AA; 36490 MW; E68A7243964380DB CRC64;

Query Match 78.6%; Score 1392.5; DB 4; Length 328;
Best Local Similarity 86.4%; Pred. No. 4.7e-123;
Matches 273; Conservative 3; Mismatches 5; Indels 35; Gaps 3;

QY 1 MAGSPTCLTIYILWLTGSAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVTNTTTP 60
1 MAGSPTCLTIYILWLTGSAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVTNTTTP 60
Db 61 VTIQEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYGIIYSSSLQQPSTQBY 120
61 VTIQEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYGIIYSSSLQQPSTQBY 120
Db 121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 5
Q8ND32
ID Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE Hypothetical protein.
GN DKFZP667F126.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Bloembergen H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7B8FC14 CRC64;
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Db 269 ---YSTVEIPKKMENP 281

RESULT 4
Q8N6Y8
ID Q8N6Y8 PRELIMINARY; PRT; 296 AA.
AC Q8N6Y8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 19A24 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027867; AAH27867.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 296 AA; 32581 MW; E85D277192494EEC CRC64;

Query Match 76.1%; Score 1349; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 5.3e-119;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTIYILWLTGSAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVTNTTTP 60
1 MAGSPTCLTIYILWLTGSAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVTNTTTP 60
Db 61 VTIQEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYGIIYSSSLQQPSTQBY 120
61 VTIQEGGTIIVTQNRNRVDFPDGGYSLKSLKKNDSGIYYGIIYSSSLQQPSTQBY 120
Db 121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
121 VLHVYHLSPKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
181 PISWRGESDMTFCICVARNPVRNFSPIARLCEGAADDPSSMVLCLLLVPLLSSL 240
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
241 FVLGLFWLFLKPERQOEYIEKKRVDCIETPNICPHSGENTYDTPHTNRTILKEDPA 300
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335
301 NTYISTVTEIPKKMENPHSLTTPDTPRLPAYENVI 335

RESULT 5
Q8ND32
ID Q8ND32 PRELIMINARY; PRT; 228 AA.
AC Q8ND32;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN DKFZP667F126.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RA Bloembergen H., Boecher M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL834424; CAD39085.1; -
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 228 AA; 25831 MW; 2B01DB70E7B8FC14 CRC64;
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Query Match      65.5%; Score 1160.5; DB 4; Length 228;
Best Local Similarity 68.1%; Pred. No. 2.4e-101;
Matches 228; Conservative 0; Mismatches 0; Indels 107; Gaps 1;

QY 1 MAGSPCTCLTIYILWOLTGSAAGPVKELVSGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPCTCLTIYILWOLTGSAAGPVKELVSGGAVTFPLKSKVKQVDSIVWTFNTTPL 18

QY 61 VTIOPEGGTIIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVGYSSSQLOPSTQRY 120
DB 19 ----- 18

QY 121 VLHVYHLKSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSL 180
DB 19 -----BHLKSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSL 73

QY 181 PISWRGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMWLLCLLLVPLL 240
DB 74 PISWRGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMWLLCLLLVPLL 133

QY 241 FVLGLFWLFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNRTILK 300
DB 134 FVLGLFWLFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNRTILK 193

QY 301 NTVYSTVEIPKXWENPHSLTTPDTPRLPAYENVI 335
DB 194 NTVYSTVEIPKXWENPHSLTTPDTPRLPAYENVI 228

RESULT 6
QBHK6 PRELIMINARY; PRT; 333 AA.
ID QBHK6
AC QBHK6;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Aorta;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK030135; BAC26801.1; -.
DR EMBL; AK030148; BAC26810.1; -.
DR EMBL; AK040678; BAC30665.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 333 AA; 37217 MW; 0CC9A0AAFEACD46E CRC64;

Query Match      46.1%; Score 817; DB 11; Length 333;
Best Local Similarity 49.6%; Pred. No. 1.2e-68;
Matches 168; Conservative 59; Mismatches 102; Indels 10; Gaps 4;

QY 1 MAGSPCTCLTIYILWOLTGSAAGPVKELVSGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MARFSTVIIFTSVLCQITVTAAGTLKKVAGALDGSVFTLNITEIKVDYVYVWTFNTTFL 60

QY 61 VTIOPEGGTIIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVGYSSSQLOPSTQRY 120
DB 61 AMVKDGG---VTSQSNKRIIVFPDGLYSMLKSQLKKNDSGAYRAEYISTSSQASLIQY 117

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QY 121 VLHVYHLKSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSL 180
DB 118 VLHVYHLKSPKVTIDROSNGKNGTCVINTLCTDQDGENVTYSWKAVQGGNQFHDGATL 177

QY 181 PISWRGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMWLLCLLLVPLL 240
DB 178 SIARSGEKQALTCMARNPVSNFSFVFPQKLCEDAATDLTSLRGLYILCFSAVLIL 237

QY 241 F--VLGLF--LWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNRTILK 296
DB 238 FAVLLTIFHTTWIKKGC---EDKKRVDHQRQEMDPLCPHLEENADYDTIPTYTEKRPE 294

QY 297 EDPANTYVSTVEIPKXWENPHSLTTPDTPRLPAYENVI 335
DB 295 EDPANTYVSTVQIPKVKVSPSSLPKPLVPRSLSPFNVI 333

RESULT 7
QB64 PRELIMINARY; PRT; 335 AA.
ID QB64
AC QB64;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel Ly9, a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402 (2002).
DR EMBL; AF467910; AAN63159.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 335 AA; 37590 MW; 85F00AABDFC8B90A0 CRC64;

Query Match      43.9%; Score 778.5; DB 11; Length 335;
Best Local Similarity 48.8%; Pred. No. 5.3e-65;
Matches 161; Conservative 55; Mismatches 101; Indels 13; Gaps 4;

QY 1 MAGSPCTCLTIYILWOLTGSAAGPVKELVSGGAVTFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MARFSTVIIFTSVLCQITVTAAGTLKKVAGALDGSVFTLNITEIKVDYVYVWTFNTTFL 60

QY 61 VTIOPEGGTIIIVTONRNRERVDPPGGYSLKSLKKNDSGIYVGYSSSQLOPSTQRY 120
DB 61 AMVKDGG---VTSQSNKRIIVFPDGLYSMLKSQLKKNDSGAYRAEYISTSSQASLIQY 117

QY 121 VLHVYHLKSPKVTMGLQSNKNGTCVTNLTCCMEHGEEDVIYTWKALGOAANESHGSL 180
DB 118 VLHVYHLKSPKVTIDROSNGKNGTCVINTLCTDQDGENVTYSWKAVQGGNQFHDGATL 177

QY 181 PISWRGSDMTFICVARNPVSRNPFSSPILARKLCEGAADDPDSSMWLLCLLLVPLL 240
DB 178 SIARSGEKQALTCMARNPVSNFSFVFPQKLCEDAATDLTSLRGLYILCFSAVLIL 237

QY 241 FVLGLF---LWFLKREOEYIEKKRVDICRETNICPHSGENTYDTIPTHTNRTILK 296
DB 238 FAVLLTIFHTTWIKKGC---EDKKRVDHQRQEMDPLCPHLEENADYDTIPTYTEKRPE 294

QY 297 EDPANTYVSTVEIPKXWENPHSLTTPDTPRLPAYENVI 335
DB 295 EDPANTYVSTVQIPKVKVSPSSLPKPLVPRSLSPFNVI 333

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RESULT 8
Q8BTL2 PRELIMINARY; PRT; 335 AA.
AC Q8BTL2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to 19A24 protein homolog.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; PubMed=12466851;
RX MEDLINE=22354683;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK089525; BAC40914.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37521 MW; 99E8802E55A98A03 CRC64;

Query Match 43.7%; Score 773.5; DB 11; Length 335;
Best Local Similarity 48.8%; Pred. No. 1.6e-64;
Matches 161; Conservative 56; Mismatches 100; Indels 13; Gaps 5;

QY 1 MAGSPTCLTLLIYILWLTGSAAGPVKELVSGVAVTPPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGTLKKGAGALDGSVFTLNLTEIKVDYVWTFNTTFL 60
QY 61 VTIOEGGTIIVTQNRNRVDPFGGYSLSKLKKNDSGIYVYGVYSSSQQPSTQRY 120
DB 61 AMVKXDG--VTSQSNKERIVFPDGLYSKLSQKKNDSGAYRAEYISTSSQASLIQY 117
QY 121 VLHYVHLSPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTKALGQAANESHNGSIL 180
DB 118 VLHYVHLSPKVTIDROSNGKTCVNLTCSDQDGENVTYSKAVGQDQFHDGATL 177
QY 181 PISRWGESDMTFICVARNPVSRNFSPIARLCKEGAADDPDSSMVLCLLLVPLLLSL 240
DB 178 SIARSGEKDQALTCHARNPVSNFSFVPFQKLCEDAATDLTSLRGILYILCFSAVLIL 237
QY 241 F--VLGLF--LWFLKREOEYIEBKRVDCIETENICPHSGENTYDTIPTHTNRTILK 296
DB 238 FAVLLTIFHTMWIKKGKGE---EDKKRVDRHQEMDPLCPHLEENADYDTIPYTKRRPE 294
QY 297 EDAPNTVYSTVEIPKPMEN---PHSLLTMP 323
DB 295 EDAPNTFYSTVQIPKVRSCPAEHLTCQP 324

Query Match 43.4%; Score 769.5; DB 11; Length 335;
Best Local Similarity 48.5%; Pred. No. 3.7e-64;
Matches 160; Conservative 56; Mismatches 101; Indels 13; Gaps 5;

QY 1 MAGSPTCLTLLIYILWLTGSAAGPVKELVSGVAVTPPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGTLKKGAGALDGSVFTLNLTEIKVDYVWTFNTTFL 60
QY 61 VTIOEGGTIIVTQNRNRVDPFGGYSLSKLKKNDSGIYVYGVYSSSQQPSTQRY 120
DB 61 AMVKXDG--VTSQSNKERIVFPDGLYSKLSQKKNDSGAYRAEYISTSSQASLIQY 117
QY 121 VLHYVHLSPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTKALGQAANESHNGSIL 180
DB 118 ALHYVYKHLSPKVTIDROSNGKTCVNLTCSDQDGENVTYSKAVGQDQFHDGATL 177
QY 181 PISRWGESDMTFICVARNPVSRNFSPIARLCKEGAADDPDSSMVLCLLLVPLLLSL 240
DB 178 SIARSGEKDQALTCHARNPVSNFSFVPFQKLCEDAATDLTSLRGILYILCFSAVLIL 237
QY 241 F--VLGLF--LWFLKREOEYIEBKRVDCIETENICPHSGENTYDTIPTHTNRTILK 296
DB 238 FAVLLTIFHTMWIKKGKGE---EDKKRVDRHQEMDPLCPHLEENADYDTIPYTKRRPE 294
QY 297 EDAPNTVYSTVEIPKPMEN---PHSLLTMP 323
DB 295 EDAPNTFYSTVQIPKVRSCPAEHLTCQP 324

RESULT 9
Q8CJ65 PRELIMINARY; PRT; 335 AA.
AC Q8CJ65;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467911; AAN63160.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 335 AA; 37493 MW; C210E9CEADC8F3EB CRC64;

Query Match 43.4%; Score 769.5; DB 11; Length 335;
Best Local Similarity 48.5%; Pred. No. 3.7e-64;
Matches 160; Conservative 56; Mismatches 101; Indels 13; Gaps 5;

QY 1 MAGSPTCLTLLIYILWLTGSAAGPVKELVSGVAVTPPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGTLKKGAGALDGSVFTLNLTEIKVDYVWTFNTTFL 60
QY 61 VTIOEGGTIIVTQNRNRVDPFGGYSLSKLKKNDSGIYVYGVYSSSQQPSTQRY 120
DB 61 AMVKXDG--VTSQSNKERIVFPDGLYSKLSQKKNDSGAYRAEYISTSSQASLIQY 117
QY 121 VLHYVHLSPKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTKALGQAANESHNGSIL 180
DB 118 ALHYVYKHLSPKVTIDROSNGKTCVNLTCSDQDGENVTYSKAVGQDQFHDGATL 177
QY 181 PISRWGESDMTFICVARNPVSRNFSPIARLCKEGAADDPDSSMVLCLLLVPLLLSL 240
DB 178 SIARSGEKDQALTCHARNPVSNFSFVPFQKLCEDAATDLTSLRGILYILCFSAVLIL 237
QY 241 F--VLGLF--LWFLKREOEYIEBKRVDCIETENICPHSGENTYDTIPTHTNRTILK 296
DB 238 FAVLLTIFHTMWIKKGKGE---EDKKRVDRHQEMDPLCPHLEENADYDTIPYTKRRPE 294
QY 297 EDAPNTVYSTVEIPKPMEN---PHSLLTMP 323
DB 295 EDAPNTFYSTVQIPKVRSCPAEHLTCQP 324

RESULT 10
Q8CJ63 PRELIMINARY; PRT; 300 AA.
AC Q8CJ63;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte cell-surface antigen isoform s.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAUB/C; TISSUE=Thymus;
RX MEDLINE=22226696; PubMed=12242590;
RA Tovar V., Del Valle J., Zapater N., Martin M., Romero X., Pizcueta P.,
RA Bosch J., Terhorst C., Engel P.;
RT "Mouse novel ly9: a new member of the expanding CD150 (SLAM) family of
RT leukocyte cell-surface receptors.";
RL Immunogenetics 54:394-402(2002).
DR EMBL; AF467911; AAN63160.1; -.
DR PIR; PT0566; PT0566.
DR MGD; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 300 AA; 33332 MW; 9948108710BEB3D CRC64;
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Query Match          36.7%; Score 651; DB 11; Length 300;
Best Local Similarity 42.4%; Pred. No. 5.1e-53;
Matches 140; Conservative 50; Mismatches 92; Indels 48; Gaps 4;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGAATPPLKSKVKQVDSIVWTFNTTFL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGLTKKVGALDGSVFTLNLTEIKVDYVWTFNTTFL 60

QY 61 VTIOPEGGTHIIVTONRRRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQRY 120
DB 61 AMVKDGG---VTSQSNKERIVFPDGLYSKMLSQLKKNDSGAYRABIYSTSQASLIQRY 117

QY 121 VLHVYHLSKPKVTMGLOQNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSIL 180
DB 118 VLHVYHLSKRPKVTIDRQSNKNGTCVINLTCTDQGENVTYSKAVGQDQFHDGATL 177

QY 181 PISRWGSDMTFICVARNPVSRNFSPIARLKLCEGAADDDPSMVLCLLVLPLLSL 240
DB 178 SIAMRSGEKDQALTCWARNPVSNFSFPPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

QY 241 FVLGLFL----WFLKREQEYIEBKRVDCRETPNI---C--PHSGENTYDTIPHTN 291
DB 238 FAVLLTIFHTTWIKR-----KEKTRRR--TKHILFHCDPQSGKSQLPACKATR 288

QY 292 RTILK 296
DB 289 AKVIK 293

RESULT 12
O15430 PRELIMINARY; PRT; 328 AA.
AC O15430;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Leukocyte antigen CD84.
GN CD84.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454416; PubMed=9310491;
RA De la Fuente M.A., Pizcueta P., Nadal M., Bosch J., Engel P.;
RT "CD84 leukocyte antigen is a new member of the Ig superfamily.";
RL Blood 90:2398-2405(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Krause S.W., Rehli M., Heinz S., Ebner R., Andreesen R.;
RT "Molecular cloning of MAX.3 antigen, a glycoprotein expressed on
macrophages, platelets and megacaryocytes.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86189202; PubMed=3008886;
RA Andreesen R., Bross K.J., Osterholz J., Emmerich F.;
RT "Human macrophage maturation and heterogeneity: analysis with a newly
generated set of monoclonal antibodies to differentiation antigens.";
RL Blood 67:1257-1264(1986).
RN [4]
RP SEQUENCE FROM N.A.
RA Palou E., Sole J., Pirotto F., Gaya A.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U82988; AAB84364.1; -.
DR EMBL; AF054815; AAF21721.1; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0006952; P: defense response; TAS.
DR GO; GO:0007156; P: homophilic cell adhesion; TAS.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal.
SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206A6D0344 CRC64;

Query Match          20.5%; Score 362.5; DB 4; Length 328;
Best Local Similarity 31.5%; Pred. No. 1.1e-25;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LWQL-----TCSAASGPVKELV---GSVGAATPPLK-SKVKQVDSIVWTFNTTFLVTIQ 64
DB 6 LWILLCLQTWPEAAGKDSIFTVNGILGESVTFPVNIQEPQVKIATSKTSVAYVTP 65

QY 65 PEGGT---IIVTONRRRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQRY 121
DB 66 GDSSTAPVVTIYHRYERHALGPNLVLSDUMEDAGYKADINTQADPYTTTKRYN 125

QY 122 LHVYHLSKPKVTMGLOQNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILP 181
DB 122 LHVYHLSKPKVTMGLOQNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILP 181

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Query Match          36.0%; Score 637.5; DB 11; Length 294;
Best Local Similarity 45.6%; Pred. No. 9.4e-52;
Matches 139; Conservative 50; Mismatches 95; Indels 21; Gaps 6;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGAATPPLKSKVKQVDSIVWTFNTTFL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGLTKKVGALDGSVFTLNLTEIKVDYVWTFNTTFL 60

QY 61 VTIOPEGGTHIIVTONRRRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQRY 120
DB 61 AMVKDGG---VTSQSNKERIVFPDGLYSKMLSQLKKNDSGAYRABIYSTSQASLIQRY 117

QY 121 VLHVYHLSKPKVTMGLOQNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSIL 180
DB 118 VLHVYHLSKRPKVTIDRQSNKNGTCVINLTCTDQGENVTYSKAVGQDQFHDGATL 177

QY 181 PISRWGSDMTFICVARNPVSRNFSPIARLKLCEGAADDDPSMVLCLLVLPLLSL 240
DB 178 SIAMRSGEKDQALTCWARNPVSNFSFPPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

QY 241 FVLGLFL----WFLKREQEYIEBKRVDCRETPNI---C--PHSGENTYDTIPHTN 291
DB 238 FAVLLTIFHTTWIKR-----KEKTRRR--TKHILFHCDPQSGKSQLPACKATR 288

QY 292 RTILK 296
DB 289 AKVIK 293

RESULT 11
O91XA0 PRELIMINARY; PRT; 294 AA.
AC O91XA0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to 19A24 protein.
GN 4930560D03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=salivary gland;
RC Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011154; AAH1154.1; -.
DR MGI; MGI:1922595; 4930560D03RIK.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 294 AA; 32782 MW; F4C88BC4CPAA1AFB CRC64;

Query Match          36.0%; Score 637.5; DB 11; Length 294;
Best Local Similarity 45.6%; Pred. No. 9.4e-52;
Matches 139; Conservative 50; Mismatches 95; Indels 21; Gaps 6;

QY 1 MAGSPCTCLTIYILWOLTSAAAGPVKELVSGVGAATPPLKSKVKQVDSIVWTFNTTFL 60
DB 1 MARFSTYIIFTSVLCQLTVAASGLTKKVGALDGSVFTLNLTEIKVDYVWTFNTTFL 60

QY 61 VTIOPEGGTHIIVTONRRRERVDPPDGGYSLKSLKKNDSGIYVYVSSSQPSTQRY 120
DB 61 AMVKDGG---VTSQSNKERIVFPDGLYSKMLSQLKKNDSGAYRABIYSTSQASLIQRY 117

QY 121 VLHVYHLSKPKVTMGLOQNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSIL 180
DB 118 VLHVYHLSKRPKVTIDRQSNKNGTCVINLTCTDQGENVTYSKAVGQDQFHDGATL 177

QY 181 PISRWGSDMTFICVARNPVSRNFSPIARLKLCEGAADDDPSMVLCLLVLPLLSL 240
DB 178 SIAMRSGEKDQALTCWARNPVSNFSFPPQKLCEDAATDLTSLRGILYILCFSAVLIL 237

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Db 126 LQIYRLGPKITQSLMASVNSTCNVTLTCSVEKEKNTYVNSPLGE-----EGNVLQ 179
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Db 180 IFQTPEDQELTCTCAQNPVSN-SDSISARQLCADIAMGFRTHHTGLLSVLAMPFLVL 238
QY 236 LLLSLFVLGLFWLKRQOEYIEKRVDCRETPNICPHSGENTEYDTTPIHNRITL 295
Db 239 ILSSVFLFLF-----KRDQAASKTITYTIMASRNTQP--AESRIYDEILQSKVLPS 290
QY 296 KEDPANTVYSTVEIPKKNPHSLTMDPTPRLFAYENVI 335
Db 291 KEEPNVTYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

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AC Q8WLP1
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DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE CD84 antigen (Leukocyte antigen).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020063; AAH20063.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 328 AA; 36871 MW; 6C9A89206A6D0344 CRC64;

Query Match 20.5%; Score 362.5; DB 7; Length 328;
Best Local Similarity 31.5%; Pred. No. 1.1e-25;
Matches 107; Conservative 55; Mismatches 143; Indels 35; Gaps 10;

QY 14 LMQ-----TGAASGPVKELV---GSVCGAVTFPLK-SKVQVDSIVTFTTPLVITQ 64
Db 6 LMLLLCLQTPWAAGKDEIFTVNGILGESVTFPVNIQRPQVKIIAIVTSKYAYVTP 65
QY 65 PEGGT---IIVQNRNRERVDPPDGGYSLKSLKKNDSGIYVGYSSLSQGPSTQEV 121
Db 66 GSETAPVVTTHRYEIRIHALGPNYLVISDLRMDAGDYKADINTQADPYTTIKYN 125
QY 122 LHVYELSKPKVTMGLOSKNGTCVTNLTCMEHGEEDVIYTWKALQAANESHNGSLP 181
Db 126 LQIYRLGPKITQSLMASVNSTCNVTLTCSVEKEKNTYVNSPLGE-----EGNVLQ 179
QY 182 ISRWGESDMTFCVARNPVSRNFPSPILARKLCEGAADDPDS-----SMVLLCLLLVP 235
Db 180 IFQTPEDQELTCTCAQNPVSN-SDSISARQLCADIAMGFRTHHTGLLSVLAMPFLVL 238
QY 236 LLLSLFVLGLFWLKRQOEYIEKRVDCRETPNICPHSGENTEYDTTPIHNRITL 295
Db 239 ILSSVFLFLF-----KRDQAASKTITYTIMASRNTQP--AESRIYDEILQSKVLPS 290
QY 296 KEDPANTVYSTVEIPKKNPHSLTMDPTPRLFAYENVI 335
Db 291 KEEPNVTYSEVQFADKMGKASTQDSKP--PGTSSYEIVI 328

RESULT 14
Q92178
ID Q92178 PRELIMINARY; PRT; 329 AA.
AC Q92178
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
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DE CD84 leukocyte antigen.
GN CD84.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneum;
RX MEDLINE=99180614; PubMed=10079287;
RA de la Fuente M.A., Tovar V., Pizcueta P., Nadal M., Bosch J.,
RT "Molecular cloning, characterization, and chromosomal localization of
RT the mouse homologue of CD84, a member of the CD2 family of cell
RT surface molecules.";
RL Immunogenetics 49:249-255(1999).
DR EMBL; AF043445; AAD02273.1; -.
DR MGD; MGI:1336885; Cd84.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
SQ SEQUENCE 329 AA; 37345 MW; 43BB1AA5AF1989E0 CRC64;

Query Match 20.5%; Score 362.5; DB 11; Length 329;
Best Local Similarity 30.5%; Pred. No. 1.1e-25;
Matches 105; Conservative 62; Mismatches 136; Indels 41; Gaps 14;

QY 11 IYILWQLTGSASGPVKELV---GSVCGAVTFPLK-SKVQVDSIVTFTTPLVITQ- 65
Db 8 IWFCLQTWSEAAAGKADPVPVNGILGESVTFLLNIQEPKIDNIATW-SQSSVAFIRPG 66
QY 66 -EGGTIIIVQNRNRERVDPPDGGYSLKSLKKNDSGIYVGYSSLSQGPSTQEVVLHV 124
Db 67 VNKAETVITQGYKGRIEIIQKVDLVIRDLRMDAGDYKADINEEN-EETITKIYLIH 125
QY 125 YEHLSKPKVTMGLOSKNGTCVTNLTCMEHGEEDVIYTWKALQAANESHNGSLPISW 184
Db 126 YRLKATPKITQSLMASVNSTCNITLTCSVEKEKDVTSWSPFGEKSN-----VLQIVH 179
QY 185 RWGESDMTFCVARNPVSRNFPSPILARKLCEGA-----ADDPSSMVLLCLLLVPL 237
Db 180 SPMQKLYTCTCAQNPVS-NSSDSVTVQOCPDTPTSPHRAVLPGGLAVFLLLIPML 238
QY 238 LSLFVLGLFWLKRQOEYIEKRVDCRETP-NICPHSGENTE---YDTIPIHNRIT 293
Db 239 AFLFPL-----YKRRDRIVLEAD--DVSKKTVYAVVSRNAQPTESRIYDEIQSKML 289
QY 294 ILKEDPANTVYSTVEIPKKNPHSLTMDP--TPRLFAYENVI 335
Db 290 SCKKDPVTTIYSSVQLSEKMKETN---MKDRSLPKALGNEIVV 329

RESULT 15
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AC Q8WLP1
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Leukocyte differentiation antigen CD84 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gaya A.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y12632; CAA73181.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 15:43:31 ; Search time 47 Seconds
(without alignments)
2237.566 Million cell updates/sec

Title: US-10-063-549-46

Perfect score: 1772

Sequence: 1 MAGSPTCLTIYLMQLTGS.....PHSLLTMPDTPRLFAVENVI 335

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : Published Applications AA:*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1772	100.0	335	US-09-989-727-253
6	1772	100.0	335	US-09-989-731-253
7	1772	100.0	335	US-09-989-732-253
8	1772	100.0	335	US-09-745-605-4
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1772	100.0	335	15	US-10-205-506-192	Sequence 192, App

ALIGNMENTS

RESULT 1
US-09-732-524-2
: Sequence 2: Application US/09732524

Patent No. US20020004193A1
; GENERAL INFORMATION ;
; APPLICANT: Khodadoust, Mehran ;
; TITLE OF INVENTION: NOVEL MP-7 PROTEIN AND NUCLEIC ACID MOLECULES ;
; TITLE OF INVENTION: AND USES THEREOF ;

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,524
FILING DATE:

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; LENGTH: 335 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-732-524-2

Query Match          100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61  VTIQPEGGTTIVTQNRNRERVDPPDGGYSILKSLKLNKDSGGIYVVGIYSSLSQOPSTQEY 120
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QY      121  VLHVYEHLSKPKVTMGLOSNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAAANESHNGSIL 180
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QY      301  NTVYSTVEIPKQKNPHSLLTMDPTPLFAYENVI 335
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Db      301  NTVYSTVEIPKQKNPHSLLTMDPTPLFAYENVI 335
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RESULT 2
US-09-989-722-253
; Sequence 253, Application US/09989722

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; Patent No. US20020072067A1
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; GENERAL INFORMATION:
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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; FILE OF INVENTION: Acids Encoding the Same
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; FILE REFERENCE: P27301C63
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; CURRENT APPLICATION NUMBER: US/09/989,722
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; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9,8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIIVLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIIVTNTTPL 60
Db 1 MAGSPCTCLTIIVLWLTGSAAGPVKELVSGVAVTFPLKSKVKQVDSIIVTNTTPL 60

QY 61 VTIOPEGGTIIIVQNRNRVDPPGGYSLKSLKNDSGIYVGYSSLSLQPSSTOY 120
Db 61 VTIOPEGGTIIIVQNRNRVDPPGGYSLKSLKNDSGIYVGYSSLSLQPSSTOY 120

QY 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSIL 180
Db 121 VLHVYEHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSIL 180

QY 181 PISRWGSDMTFICVARNPVSRNFSPIILARKLCEGAADDPSSMWLLCLLLVPLLSL 240
Db 181 PISRWGSDMTFICVARNPVSRNFSPIILARKLCEGAADDPSSMWLLCLLLVPLLSL 240

QY 241 FVLGFLPLFLKREOEYIEEKRVYDICTETNCPHSGENTYDTIPIHTNRTILKEDPA 300
Db 241 FVLGFLPLFLKREOEYIEEKRVYDICTETNCPHSGENTYDTIPIHTNRTILKEDPA 300

QY 301 NTVYSTVETIPKKWENPHSLTTPDTPLRFAYENVI 335
Db 301 NTVYSTVETIPKKWENPHSLTTPDTPLRFAYENVI 335

RESULT 3
US-09-989-723-253.
; Sequence 253, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9,8e-168; Mismatches 0; Indels 0; Gaps 0;
Matches 335; Conservative 0;

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Db 1 MAGSPTCLTIYILWQLTGSAAAGPVKELVSGVGGAVTFPLKSKVKQVDSIVWTFNTTFL 60

Qy 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKQKQDSGIYYVGIYSSSLQQPSTQY 120
Db 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKQKQDSGIYYVGIYSSSLQQPSTQY 120

Qy 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEDVIVTKALGQAANESHNGSL 180
Db 121 VLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEDVIVTKALGQAANESHNGSL 180

Qy 181 PISRWGESDMTFFICVARNPVSRNFSPIILARKLCEGAADDPDSSMVLCLLLVPLLSL 240
Db 181 PISRWGESDMTFFICVARNPVSRNFSPIILARKLCEGAADDPDSSMVLCLLLVPLLSL 240

Qy 241 FVLGLFPLKREOEYIEKKRVDIQRETPNICPHSGENTYDTIPTHNRTILKEDPA 300
Db 241 FVLGLFPLKREOEYIEKKRVDIQRETPNICPHSGENTYDTIPTHNRTILKEDPA 300

Qy 301 NTVYSTVEIPKKMNPMSLTMPTDPRLFAYENVI 335
Db 301 NTVYSTVEIPKKMNPMSLTMPTDPRLFAYENVI 335

RESULT 4
US-09-989-279-253
; Sequence 253, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS Encoding the Same
FILE REFERENCE: P2730PIC56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9,8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSPCTCLTIYILWOLGTSAAGPVKELVSGVGGAVTFLKSKVKQVDSIVVTFNTTTL 60
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Qy 241 FVLGLFLWFLKRRQEQYEIEKKRVDCRETNPICPHSGENTYDTPHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKRRQEQYEIEKKRVDCRETNPICPHSGENTYDTPHTNRTILKEDPA 300
Qy 301 NTYISTVEIPKXKNPHSLLTWPDTPRLPAYENVI 335
Db 301 NTYISTVEIPKXKNPHSLLTWPDTPRLPAYENVI 335

RESULT 5
US-09-989-727-253
; Sequence 253 Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Zhang, Zemin
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;; PRIOR APPLICATION NUMBER: 60/089600
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;; PRIOR FILING DATE: 1998-06-18
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;; PRIOR APPLICATION NUMBER: 60/090696
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;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 9.8e-168;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAGSPTCLTLYILWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTTPL 60
Db 1 MAGSPTCLTLYILWLTGSAASGPVKELVSGVAVTFPLKSKVKQVDSIVTWTFTTPL 60
Qy 61 VTIOPEGTTIIVTQNRNRERVDFFDGGYSLKSLKKNDSGIYVYGVYSSLSLQOPSTOEY 120
Db 61 VTIOPEGTTIIVTQNRNRERVDFFDGGYSLKSLKKNDSGIYVYGVYSSLSLQOPSTOEY 120
Qy 121 VLHVYHLKSKPKVTMTGLQSNKNGTCVTNLTCCMEHGVEDVIYTWKALQOANESHGSL 180
Db 121 VLHVYHLKSKPKVTMTGLQSNKNGTCVTNLTCCMEHGVEDVIYTWKALQOANESHGSL 180

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;

	Matches	335;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MAGSPTCLTIYILWOLTGSAAGPVKVLVGSVGGA	VTPFLKSKVKQVD	SIVVTFTTPL	60					
Dd	1	MAGSPTCLTIYILWOLTGSAAGPVKVLVGSVGGA	VTPFLKSKVKQVD	SIVVTFTTPTL	60					
Qy	61	VTIQPEGGTIIVTQNRNRRVDPDGGYSIKLSKLKND	SGIYYVGYSSSQLOQPSTQEY	120						
Dd	61	VTIQPEGGTIIVTQNRNRRVDPDGGYSIKLSKLKND	SGIYYVGYSSSQLOQPSTQEY	120						
Qy	121	VLHVYEHLSPKVMTGLQSNKNGTCVTNLITCCMEHGEEDVI	YTWKALGQAANESHNGSIL	180						
Dd	121	VLHVYEHLSPKVMTGLQSNKNGTCVTNLITCCMEHGEEDVI	YTWKALGQAANESHNGSIL	180						
Qy	181	PISWRGESDMTFICVARNPVSRNFSSPILARKLCEGAADPDSSMWLLC	LILLVPLLISL	240						
Dd	181	PISWRGESDMTFICVARNPVSRNFSSPILARKLCEGAADPDSSMWLLC	LILLVPLLISL	240						
Qy	241	FVLGLFWFLFKRQEYIEBKRVDI	CRTPNICPHSGENTVEDTIPHTNRILKEDPA	300						
Dd	241	FVLGLFWFLFKRQEYIEBKRVDI	CRTPNICPHSGENTVEDTIPHTNRILKEDPA	300						
Qy	301	NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI	335							
Dd	301	NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI	335							
RESULT 7										
US-09-989-732-253										
; Sequence 253, Application US/09989732										
; Patent No. US20020123463A1										
GENERAL INFORMATION:										
; APPLICANT: Ashkenazi, Avi J.										
; APPLICANT: Baker, Kevin P.										
; APPLICANT: Botstein, David										
; APPLICANT: Desnoyers, Luc										
; APPLICANT: Eaton, Dan L.										
; APPLICANT: Ferrara, Napoleone										
; APPLICANT: Fong, Sherman										
; APPLICANT: Gerber, Hanspeter										
; APPLICANT: Gerritsen, Mary E.										
; APPLICANT: Goddard, Audrey										
; APPLICANT: Godowski, Paul J.										
; APPLICANT: Grimaldi, J. Christopher										
; APPLICANT: Gurney, Austin L.										
; APPLICANT: Kljavin, Ivar J.										
; APPLICANT: Napier, Mary A.										
; APPLICANT: Pan, James										
; APPLICANT: Paoni, Nicholas F.										
; APPLICANT: Roy, Margaret Ann										
; APPLICANT: Stewart, Timothy A.										
; APPLICANT: Tumas, Daniel										
; APPLICANT: Watanabe, Colin K.										
; APPLICANT: Williams, P. Mickey										
; APPLICANT: Wood, William I.										
; APPLICANT: Zhang, Zemin										
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic										
TITLE OF INVENTION: Acids Encoding the Same										
FILE REFERENCE: P2730P1C57										
CURRENT APPLICATION NUMBER: US/09/989,732										
CURRENT FILING DATE: 2001-11-19										
PRIOR APPLICATION NUMBER: 60/049787										
PRIOR FILING DATE: 1997-06-16										
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PRIOR FILING DATE: 1997-10-17										
PRIOR APPLICATION NUMBER: 60/065186										
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PRIOR FILING DATE: 1997-11-24										
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PRIOR FILING DATE: 1998-02-25										

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3	PRIOR FILING DATE: 1998-06-17	
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63	PRIOR FILING DATE: 1998-06-26	
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70	PRIOR APPLICATION NUMBER: 60/091544	
71	PRIOR FILING DATE: 1998-07-01	
72	PRIOR APPLICATION NUMBER: 60/091519	
73	PRIOR FILING DATE: 1998-07-02	

;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYLQLTGSAAGVPKELVSGVGAVTFFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPTCLTLLIYLQLTGSAAGVPKELVSGVGAVTFFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDGSIYVYGIYSSSLQQPSTOEY 120
DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDGSIYVYGIYSSSLQQPSTOEY 120
QY 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180
DB 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180
QY 181 PISRWGSDMTFICVARNPVSRNFSFILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240
DB 181 PISRWGSDMTFICVARNPVSRNFSFILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
QY 301 NTVSTVEIPKKNPHSLTTPDTPRLPAYENVI 335
DB 301 NTVSTVEIPKKNPHSLTTPDTPRLPAYENVI 335

RESULT 8
US-09-745-605-4
; Sequence 4, Application US/09745605
; Patent No. US20020123617A1
; GENERAL INFORMATION:
; APPLICANT: Spaulding, Gary C.
; APPLICANT: Finger, Joshua N.
; TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUPERFAMILY MEMBERS APEX-1, APEX-2,
; FILE OF INVENTION: AND APEX-3 AND USES THEREOF
; FILE REFERENCE: DB13NP
; CURRENT APPLICATION NUMBER: US/09/745,605
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/172,025
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-745-605-4

Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPTCLTLLIYLQLTGSAAGVPKELVSGVGAVTFFPLKSKVKQVDSIVWTFNTTPL 60
DB 1 MAGSPTCLTLLIYLQLTGSAAGVPKELVSGVGAVTFFPLKSKVKQVDSIVWTFNTTPL 60
QY 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDGSIYVYGIYSSSLQQPSTOEY 120
DB 61 VTIOPEGGTIIVTQNRNRVDFPDGGYSLKSLKNDGSIYVYGIYSSSLQQPSTOEY 120

QY 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180
DB 121 VLHVYHLSKPKVTWGLQSNKNGTCVTNLTCCMEHGEDVITYWKALQOANESHNGSIL 180
QY 181 PISRWGSDMTFICVARNPVSRNFSFILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240
DB 181 PISRWGSDMTFICVARNPVSRNFSFILARKLCEGAADDPDSSMWLLCLLLVPLLLSL 240
QY 241 FVLGLFLWFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
DB 241 FVLGLFLWFLKREOEYIEEKRVDCRETENICPHSGENTYDTIHTNRTILKEDPA 300
QY 301 NTVSTVEIPKKNPHSLTTPDTPRLPAYENVI 335
DB 301 NTVSTVEIPKKNPHSLTTPDTPRLPAYENVI 335

RESULT 9
US-09-991-073-253
; Sequence 253, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaudo, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607


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; PRIOR FILING DATE: 1998-07-09
Query Match      100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9,8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGSPCTCLTIYILWLTGSAASGPKVKGSLKNDGSIYVYVYSSLSQPSY 60
Db 1 MAGSPCTCLTIYILWLTGSAASGPKVKGSLKNDGSIYVYVYSSLSQPSY 60
QY 61 VTIOPEGGTIIYQNRNRRVDFPGGYSLKSLKNDGSIYVYVYSSLSQPSY 120
Db 61 VTIOPEGGTIIYQNRNRRVDFPGGYSLKSLKNDGSIYVYVYSSLSQPSY 120
QY 121 VLVVYEHLSKPKVTWGLSNKNGTCVNLTCCEHGEEDVIYTKALGOANESHNGSIL 180
Db 121 VLVVYEHLSKPKVTWGLSNKNGTCVNLTCCEHGEEDVIYTKALGOANESHNGSIL 180
QY 181 PISRWGSDMTFFICVARNPVSRNFSPI LARKLCEGAADDPDSSWVLLCLLLVPLLSL 240
Db 181 PISRWGSDMTFFICVARNPVSRNFSPI LARKLCEGAADDPDSSWVLLCLLLVPLLSL 240
QY 241 FVLGLFLWFLKREGEYIEEKRVYDICTETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
Db 241 FVLGLFLWFLKREGEYIEEKRVYDICTETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
QY 301 NTIVSTVETPKWENPHSLTTPDTPRLFAYENVI 335
Db 301 NTIVSTVETPKWENPHSLTTPDTPRLFAYENVI 335

RESULT 10
US-09-990-442-253
; Sequence 253 Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR FILING DATE: 1998-02-25
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Qy	181	PISWRGESDMFTFCVARNPSVRNPF		
Dd	181	PISWRGESDMFTFCVARNPSVRNPF		
Qy	241	FVLGLFLWLKRQEVEIEKKRV		
Dd	241	FVLGLFLWLKRQEVEIEKKRV		
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RESULT 11
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; Patent No. US20201312253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Borstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhapp, Zemin

;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC17
;; CURRENT APPLICATION NUMBER: US/09/991,163
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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT FILING DATE: 2001-11-14
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Sequence 253, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deanovaya, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

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Query Match 100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 PISWRGESDMTFICVARNPVSRNFPSPILARKLCEGAADPDSSWLLCLLLVPLLSL 240
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Qy 301 NTVYSTVEIPKXMPHSHLLTMDTPRLFAYENVI 335
Db 301 NTVYSTVEIPKXMPHSHLLTMDTPRLFAYENVI 335

RESULT 13
US-09-990-456-253
; Sequence 253, Application US/09990456

Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 1772; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 9.8e-168;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VTIOPEGGTIIYTONRNRERVDPPGGYSLKLSKLNKDSGIIYVYGYSSSLQOQSTOEY 120

QY 121 VLHVYHLSKPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOANESHNGSIL 180
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QY 181 PISRWGSDMTFICVARNPVSRRNFPSPILARKLCEGAADDPDSSMWLLCLLLVPLLJSL 240
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QY 241 FVLGLFLWFLKRRQOEYIEEKRVVDICRETPNICPHSGENTYDTIPIHTNRTILKEDPA 300
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QY 301 NTVYSTVEIPKKMENPHSLTTPDTPRLFAYENVI 335
Db 301 NTVYSTVEIPKKMENPHSLTTPDTPRLFAYENVI 335

RESULT 14
US-09-989-721-253
; Sequence 253, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanovs, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
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67 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 1772; DB 9; Length 335;

Best Local Similarity 100.0%; Pred. No. 9,8e-168;

Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VLHVYHLSPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
Db 121 VLHVYHLSPKVTMTGLQSNKNGTCVTNLTCCMEHGEEDVIYTKALGOAANESHNGSIL 180
QY 181 PISRWGSDMTFICVARNPVSRNFPSSPILARKLCEGAADPDSSMWLLCLLLVPLLSL 240
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QY 301 NTVYSTVETPKKWNPHSLTTPDTPRLFAVENVI 335
Db 301 NTVYSTVETPKKWNPHSLTTPDTPRLFAVENVI 335
RESULT 15
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; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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5	PRIOR FILING DATE: 1998-06-18	
6	PRIOR APPLICATION NUMBER: 60/089907	
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64	PRIOR APPLICATION NUMBER: 60/091478	
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66	PRIOR APPLICATION NUMBER: 60/091544	
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68	PRIOR APPLICATION NUMBER: 60/091519	
69	PRIOR FILING DATE: 1998-07-02	
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